(51) International Patent Classification ⁶ :	A2	(11) International Publication Number:	WO 99/06552
C12N 15/12, C07K 14/47, C12N 15/10, 15/11		(43) International Publication Date:	11 February 1999 (11.02.99)

(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN BRAIN

(57) Abstract

The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.

5' ESTs FOR SECRETED PROTEINS EXPRESSED IN BRAIN

Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer tremendous promise for the understanding, diagnosis, and treatment of human diseases. In addition, probes capable of specifically hybridizing to loci distributed throughout the human genome find applications in the construction of high resolution chromosome maps and in the identification of individuals.

In the past, the characterization of even a single human gene was a painstaking process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA sequencing, and computer technology have merged to greatly accelerate the rate at which human genes can be isolated, sequenced, mapped, and characterized. Cloning vectors such as yeast artificial chromosomes (YACs) and bacterial artificial chromosomes (BACs) are able to accept DNA inserts ranging from 300 to 1000 kilobases (kb) or 100-400 kb in length respectively, thereby facilitating the manipulation and ordering of DNA sequences distributed over great distances on the human chromosomes. Automated DNA sequencing machines permit the rapid sequencing of human genes. Bioinformatics software enables the comparison of nucleic acid and protein sequences, thereby assisting in the characterization of human gene products.

Currently, two different approaches are being pursued for identifying and characterizing the genes distributed along the human genome. In one approach, large fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading frames in these genomic sequences are identified using bioinformatics software. However, this approach entails sequencing large stretches of human DNA which do not encode proteins in order to find the protein encoding sequences scattered throughout the genome. In addition to requiring extensive sequencing, the bioinformatics software may mischaracterize the genomic sequences obtained. Thus, the software may produce false positives in which non-coding DNA is mischaracterized as coding DNA or false negatives in which coding DNA is mislabeled as non-coding DNA.

An alternative approach takes a more direct route to identifying and characterizing human genes. In this approach, complementary DNAs (cDNAs) are synthesized from isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach,

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sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended cDNAs which include sequences adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters.

In the past, these short EST sequences were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs. (Adams *et al., Nature* 377:3-174, 1996; Hillier *et al., Genome Res.* 6:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been obtained, the reported sequences typically correspond to coding sequences and do not include the full 5' untranslated region of the mRNA from which the cDNA is derived. Such incomplete sequences may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences derived from the 5' ends of mRNAs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. Of the 50,000-100,000 protein coding genes, those genes encoding proteins which are secreted from the cell in which they are synthesized, as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often

involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells.

In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon-α, interferon-β, interferon-γ, and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy induced neutropenia and multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a particularly valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded by the signal sequences located at the 5' ends of the coding sequences of genes encoding secreted proteins. Because these signal peptides will direct the extracellular secretion of any protein to which they are operably linked, the signal sequences may be exploited to direct the efficient secretion of any protein by operably linking the signal sequences to a gene encoding the protein for which secretion is desired. In addition, portions of signal sequences may also be used to direct the intracellular import of a peptide or protein of interest. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cell in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches

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have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross, *et al., Nature Genetics* 6: 236-244, 1994). The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock *et al., Genome Res.* 6:327-335, 1996). Both of these approaches have their limits due to a lack of specificity or of comprehensiveness.

The present 5' ESTs may be used to efficiently identify and isolate upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. (Theil, *BioFactors* 4:87-93, 1993). Once identified and characterized, these regulatory regions may be utilized in gene therapy or protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5' ends of secretory protein genes may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding sequences of genes encoding secretory proteins.

Summary of the Invention

The present invention relates to purified, isolated, or recombinant ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. The term "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. These sequences will be referred to hereinafter as "5' ESTs." As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5' EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4-10^6 fold purification of the native message.

Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the 5' EST is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the 5' ESTs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5' ESTs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched 5' ESTs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched 5' ESTs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

"Stringent", moderate," and "low" hybridization conditions are as defined in Example 29.

Unless otherwise indicated, a "complementary" sequence is fully complementary.

Thus, 5' ESTs in cDNA libraries in which one or more 5' ESTs make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant 5' ESTs" as defined herein. Likewise, 5' ESTs in a population of plasmids in which one or more 5' EST of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are " enriched recombinant 5' ESTs" as defined herein. However, 5' ESTs in cDNA libraries in which 5' ESTs constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in

which backbone molecules having a 5' EST insert are extremely rare, are not "enriched recombinant 5' ESTs."

In particular, the present invention relates to 5' ESTs which are derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Such 5' ESTs include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the genes from which the 5' ESTs are derived. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The 5' ESTs of the present invention have several important applications. For example, they may be used to obtain and express cDNA clones which include the full protein coding sequences of the corresponding gene products, including the authentic translation start sites derived from the 5' ends of the coding sequences of the mRNAs from which the 5' ESTs are derived. These cDNAs will be referred to hereinafter as "full length cDNAs." These cDNAs may also include DNA derived from mRNA sequences upstream of the translation start site. The full length cDNA sequences may be used to express the proteins corresponding to the 5' ESTs. As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating or

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controlling a variety of human conditions.. The 5' ESTs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes the mRNA from which the 5' EST was derived.

Alternatively, the 5' ESTs may be used to obtain and express extended cDNAs encoding portions of the secreted protein. The portions may comprise the signal peptides of the secreted proteins or the mature proteins generated when the signal peptide is cleaved off. The portions may also comprise polypeptides having at least 10 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. Alternatively, the portions may comprise at least 15 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In some embodiments, the portions may comprise at least 25 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In other embodiments, the portions may comprise at least 40 amino acids encoded by the extended cDNAs or full length cDNAs.

Antibodies which specifically recognize the entire secreted proteins encoded by the extended cDNAs, full length cDNAs, or fragments thereof having at least 10 consecutive amino acids, at least 15 consecutive amino acids, at least 25 consecutive amino acids, or at least 40 consecutive amino acids may also be obtained as described below. Antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the signal peptides encoded by the extended cDNAs or full length cDNAs may also be obtained.

In some embodiments, the extended cDNAs obtained using the 5' ESTs include the signal sequence. In other embodiments, the extended cDNAs obtained using the 5' ESTs may include the full coding sequence for the mature protein (*i.e.* the protein generated when the signal polypeptide is cleaved off). In addition, the extended cDNAs obtained using the 5' ESTs may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression.

As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the extended cDNAs or full length cDNAs obtained using the 5' ESTs may be useful in treating or controlling a variety of human conditions.

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The 5' ESTs (or cDNAs or genomic DNAs obtained therefrom) may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the 5' ESTs. In addition, the present invention is useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the 5' ESTs, such as promoters or upstream regulatory sequences.

Finally, the present invention may also be used for gene therapy to control or treat genetic diseases. Signal peptides may also be fused to heterologous proteins to direct their extracellular secretion.

Bacterial clones containing Bluescript plasmids having inserts containing the 5' ESTs of the present invention (SEQ ID NOs: 38-270 are presently stored at 80°C in 4% (v/v) glycerol in the inventor's laboratories under the designations listed next to the SEQ ID NOs in II). The inserts may be recovered from the deposited materials by growing the appropriate clones on a suitable medium. The Bluescript DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

One aspect of the present invention is a purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-270 or having a sequence complementary thereto. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary thereto.

Yet another aspect of the present invention is a purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-270 or one of the sequences complementary thereto. In one embodiment, the nucleic acid is recombinant.

A further aspect of the present invention is a purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-270. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-270.

Still another aspect of the present invention is a method of making a cDNA encoding a human secretory protein, said human secretory protein being partially encoded by one of SEQ ID NOs 38-270, comprising the steps of contacting a collection of mRNA molecules from human cells with a primer comprising at least 15 consecutive nucleotides of a sequence complementary to one of SEQ ID NOs: 38-270; hybridizing said primer to an mRNA in said collection that encodes said protein; reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA; making a second cDNA strand complementary to said first cDNA strand; and isolating the resulting cDNA encoding said protein comprising said first cDNA strand and said second cDNA strand.

Another aspect of the invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the

cDNA comprises the full protein coding sequence of said protein which sequence is partially included in one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is a method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-270, comprising the steps of obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-270; contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-270 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA; identifying a cDNA which hybridizes to said detectable probe; and isolating said cDNA which hybridizes to said probe.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is a method of making a cDNA comprising one of the sequence of SEQ ID NOs: 38-270, comprising the steps of contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA; hybridizing said first primer to said polyA tail; reverse transcribing said mRNA to make a first cDNA strand; making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-270; and isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

In one embodiment of the method described in the two paragraphs above, the second cDNA strand is made by contacting said first cDNA strand with a first pair of primers, said

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first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-270 and a third primer having a sequence therein which is included within the sequence of said first primer; performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product; contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NOs: 38-270 , and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and performing a second polymerase chain reaction, thereby generating a second PCR product.

One aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is the method described four paragraphs above in which the second cDNA strand is made by contacting said first cDNA strand with a second primer comprising at least 15 consecutive nucleotides of the sequences of SEQ ID NOs: 38-270; hybridizing said second primer to said first strand cDNA; and extending said hybridized second primer to generate said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-270 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in of one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is a method of making a protein comprising one of the sequences of SEQ ID NOs: 271-503, comprising the steps of obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NOs: 38-270; inserting said cDNA in an expression vector such that said cDNA is

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operably linked to a promoter; introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and isolating said protein.

Another aspect of the present invention is an isolated protein obtainable by the method described in the preceding paragraph.

Another aspect of the present invention is a method of obtaining a promoter DNA comprising the steps of obtaining DNAs located upstream of the nucleic acids of SEQ ID NOs: 38-270 or the sequences complementary thereto; screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and isolating said DNA comprising said identified promoter. In one embodiment, the obtaining step comprises chromosome walking from said nucleic acids of SEQ ID NOs: 38-270 or sequences complementary thereto. In another embodiment, the screening step comprises inserting said upstream sequences into a promoter reporter vector. In another embodiment, the screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

Another aspect of the present invention is an isolated promoter obtainable by the method described above.

Another aspect of the present invention is an isolated or purified protein comprising one of the sequences of SEQ ID NOs: 271-503.

Another aspect of the present invention is the inclusion of at least one of the sequences of SEQ ID NOs: 38-270, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-270, or a fragment thereof of at least 15 consecutive nucleotides in an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length. In one embodiment, the array includes at least two of the sequences of SEQ ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or fragments thereof of at least 15 consecutive nucleotides. In another embodiment, the array includes at least five of the sequences of SEQ ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or fragments thereof of at least 15 consecutive nucleotides.

Another aspect of the present invention is a promoter having a sequence selected from the group consisting of SEQ ID NOs: 31, 34, and 37.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they derived.

Figure 2 shows the distribution of Von Heijne scores for 5' ESTs in each of the categories described herein and the probability that these 5' ESTs encode a signal peptide.

Figure 3 summarizes a general method used to clone and sequence extended cDNAs containing sequences adjacent to 5' ESTs.

Figure 4 (description of promoters structure isolated from SignalTag 5' ESTs) provides a schematic description of promoters isolated and the way they are assembled with the corresponding 5' tags.

Detailed Description of the Preferred Embodiment

Table IV is an analysis of the 43 amino acids located at the N terminus of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Table V shows the distribution of 5' ESTs in each category described herein and the number of 5' ESTs in each category having a given minimum Von Heijne's score.

Table VI shows the distribution of 5' ESTs in each category described herein with respect to the tissue from which the 5' ESTs of the corresponding mRNA were obtained.

Table VII describes the transcription factor binding sites present in each of these promoters.

I. General Methods for Obtaining 5' ESTs derived from mRNAs with intact 5' ends

In order to obtain the 5' ESTs of the present invention, mRNAs with intact 5' ends must be obtained. Currently, there are two approaches for obtaining such mRNAs with intact 5' ends as described below: either chemical (1) or enzymatic (2).

1. Chemical Methods for Obtaining mRNAs having Intact 5' Ends

One of these approaches is a chemical modification method involving derivatization of the 5' ends of the mRNAs and selection of the derivatized mRNAs. The 5' ends of eukaryotic mRNAs possess a structure referred to as a "cap" which comprises a guanosine

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methylated at the 7 position. The cap is joined to the first transcribed base of the mRNA by a 5', 5'-triphosphate bond. In some instances, the 5' guanosine is methylated in both the 2 and 7 positions. Rarely, the 5' guanosine is trimethylated at the 2, 7 and 7 positions. In the chemical method for obtaining mRNAs having intact 5' ends, the 5' cap is specifically derivatized and coupled to a reactive group on an immobilizing substrate. This specific derivatization is based on the fact that only the ribose linked to the methylated guanosine at the 5' end of the mRNA and the ribose linked to the base at the 3' terminus of the mRNA, possess 2', 3'-cis diols.

Optionally, the 2', 3'-cis diol of the 3' terminal ribose may be chemically modified, substituted, converted, or eliminated, leaving only the ribose linked to the methylated guanosine at the 5' end of the mRNA with a 2', 3'-cis diol. A variety of techniques are available for eliminating the 2', 3'-cis diol on the 3' terminal ribose. For example, controlled alkaline hydrolysis may be used to generate mRNA fragments in which the 3' terminal ribose is a 3'-phosphate, 2'-phosphate or (2', 3')-cyclophosphate. Thereafter, the fragment which includes the original 3' ribose may be eliminated from the mixture through chromatography on an oligodT column. Alternatively, a base which lacks the 2', 3'-cis diol may be added to the 3' end of the mRNA using an RNA ligase such as T4 RNA ligase. Example 1 below describes a method for ligation of a nucleoside diphosphate to the 3' end of messenger RNA.

EXAMPLE 1

Ligation of the Nucleoside Diphosphate pCp to the 3' End of mRNA.

One μg of RNA was incubated in a final reaction medium of 10 μl in the presence of 5 U of T$_4$ phage RNA ligase in the buffer provided by the manufacturer (Gibco - BRL), 40 U of the RNase inhibitor RNasin (Promega) and, 2 μl of ^{32}pCp (Amersham #PB 10208). The incubation was performed at 37°C for 2 hours or overnight at 7-8°C.

Following modification or elimination of the 2', 3'-cis diol at the 3' ribose, the 2', 3'-cis diol present at the 5' end of the mRNA may be oxidized using reagents such as NaBH$_4$, NaBH$_3$CN, or sodium periodate, thereby converting the 2', 3'-cis diol to a dialdehyde. Example 2 describes the oxidation of the 2', 3'-cis diol at the 5' end of the mRNA with sodium periodate.

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EXAMPLE 2

Oxidation of 2', 3'-cis diol at the 5' End of the mRNA with Sodium Periodate

0.1 OD unit of either a capped oligoribonucleotide of 47 nucleotides (including the cap) or an uncapped oligoribonucleotide of 46 nucleotides were treated as follows. The oligoribonucleotides were produced by *in vitro* transcription using the transcription kit "AmpliScribe T7" (Epicentre Technologies). As indicated below, the DNA template for the RNA transcript contained a single cytosine. To synthesize the uncapped RNA, all four NTPs were included in the *in vitro* transcription reaction. To obtain the capped RNA, GTP was replaced by an analogue of the cap, m7G(5')ppp(5')G. This compound, recognized by the polymerase, was incorporated into the 5' end of the nascent transcript during the initiation of transcription but was not incorporated during the extension step. Consequently, the resulting RNA contained a cap at its 5' end. The sequences of the oligoribonucleotides produced by the *in vitro* transcription reaction were:

+Cap:

5'm7GpppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3' (SEQ ID NO:1)

-Cap:

5'-pppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3' (SEQ ID NO:2)

The oligoribonucleotides were dissolved in 9 µl of acetate buffer (0.1 M sodium acetate, pH 5.2) and 3 µl of freshly prepared 0.1 M sodium periodate solution. The mixture was incubated for 1 hour in the dark at 4°C or room temperature. Thereafter, the reaction was stopped by adding 4 µl of 10% ethylene glycol. The product was ethanol precipitated, resuspended in at least 10 µl of water or appropriate buffer and dialyzed against water.

The resulting aldehyde groups may then be coupled to molecules having a reactive amine group, such as hydrazine, carbazide, thiocarbazide or semicarbazide groups, in order to facilitate enrichment of the 5' ends of the mRNAs. Molecules having reactive amine groups which are suitable for use in selecting mRNAs having intact 5' ends include avidin, proteins, antibodies, vitamins, ligands capable of specifically binding to receptor molecules, or oligonucleotides. Example 3 below describes the coupling of the resulting dialdehyde to biotin.

EXAMPLE 3

Coupling of the Dialdehyde at the 5' End of Transcripts with Biotin

The oxidation product obtained in Example 2 was dissolved in 50 μl of sodium acetate at a pH between 5 and 5.2 and 50 μl of freshly prepared 0.02 M solution of biotin
5   hydrazide in a methoxyethanol/water mixture (1:1) of formula:
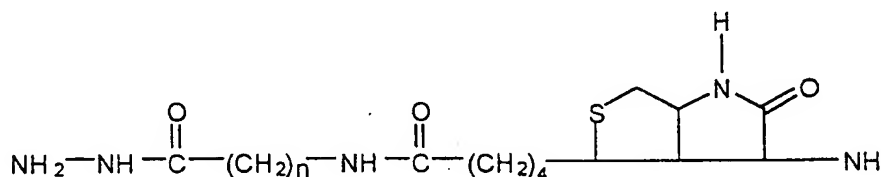
In the compound used in these experiments, n=5. However, it will be appreciated that
10   other commercially available hydrazides may also be used, such as molecules of the above formula in which n varies from 0 to 5. The mixture was then incubated for 2 hours at 37°C, precipitated with ethanol and dialyzed against distilled water. Example 4 demonstrates the specificity of the biotinylation reaction.

15   **EXAMPLE 4**

Specificity of Biotinylation of Capped Transcripts

The specificity of the biotinylation for capped mRNAs was evaluated by gel electrophoresis of the following samples:

Sample 1. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2
20   and labeled with ^{32}pCp as described in Example 1.

Sample 2. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Sample 3. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2 and
25   labeled with ^{32}pCp as described in Example 1.

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Sample 4. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Samples 1 and 2 had identical migration rates, demonstrating that the uncapped
5   RNAs were not oxidized and biotinylated.   Sample 3 migrated more slowly than Samples 1 and 2, while Sample 4 exhibited the slowest migration. The difference in migration of the RNAs in Samples 3 and 4 demonstrates that the capped RNAs were specifically biotinylated.

In some cases, mRNAs having intact 5′ ends may be enriched by binding the molecule containing a reactive amine group to a suitable solid phase substrate such as the inside of the
10   vessel containing the mRNAs, magnetic beads, chromatography matrices, or nylon or nitrocellulose membranes. For example, where the molecule having a reactive amine group is biotin, the solid phase substrate may be coupled to avidin or streptavidin. Alternatively, where the molecule having the reactive amine group is an antibody or receptor ligand, the solid phase substrate may be coupled to the cognate antigen or receptor. Finally, where the
15   molecule having a reactive amine group comprises an oligonucleotide, the solid phase substrate may comprise a complementary oligonucleotide.

The mRNAs having intact 5′ ends may be released from the solid phase following the enrichment procedure. For example, where the dialdehyde is coupled to biotin hydrazide and the solid phase comprises streptavidin, the mRNAs may be released from the solid phase by
20   simply heating to 95 degrees Celsius in 2% SDS. In some methods, the molecule having a reactive amine group may also be cleaved from the mRNAs having intact 5′ ends following enrichment. Example 5 describes the capture of biotinylated mRNAs with streptavidin coated beads and the release of the biotinylated mRNAs from the beads following enrichment.

25   **EXAMPLE 5**

Capture and Release of Biotinylated mRNAs Using Streptavidin Coated Beads

The streptavidin coated magnetic beads were prepared according to the manufacturer's instructions (CPG Inc., USA). The biotinylated mRNAs were added to a hybridization buffer (1.5 M NaCl, pH 5 - 6). After incubating for 30 minutes, the unbound
30   and nonbiotinylated material was removed. The beads were then washed several times in

18

water with 1% SDS. The beads thus obtained were incubated for 15 minutes at 95°C in water containing 2% SDS.

Example 6 demonstrates the efficiency with which biotinylated mRNAs were recovered from the streptavidin coated beads.

EXAMPLE 6

Efficiency of Recovery of Biotinylated mRNAs

The efficiency of the recovery procedure was evaluated as follows. Capped RNAs were labeled with ^{32}pCp, oxidized, biotinylated and bound to streptavidin coated beads as described above. Subsequently, the bound RNAs were incubated for 5, 15 or 30 minutes at 95°C in the presence of 2% SDS.

The products of the reaction were analyzed by electrophoresis on 12% polyacrylamide gels under denaturing conditions (7 M urea). The gels were subjected to autoradiography. During this manipulation, the hydrazone bonds were not reduced.

Increasing amounts of nucleic acids were recovered as incubation times in 2% SDS increased, demonstrating that biotinylated mRNAs were efficiently recovered.

In an alternative method for obtaining mRNAs having intact 5' ends, an oligonucleotide which has been derivatized to contain a reactive amine group is specifically coupled to mRNAs having an intact cap. Preferably, the 3' end of the mRNA is blocked prior to the step in which the aldehyde groups are joined to the derivatized oligonucleotide, as described above, so as to prevent the derivatized oligonucleotide from being joined to the 3' end of the mRNA. For example, pCp may be attached to the 3' end of the mRNA using T4 RNA ligase as described in example 1. However, as discussed above, blocking the 3' end of the mRNA is an optional step. Derivatized oligonucleotides may be prepared as described in Example 7.

EXAMPLE 7

Derivatization of Oligonucleotides

An oligonucleotide phosphorylated at its 3' end was converted to a 3' hydrazide in 3' by treatment with an aqueous solution of hydrazine or of dihydrazide of the formula $H_2N(R1)NH_2$ at about 1 to 3 M, and at pH 4.5 at a temperature of 8°C overnight. This

incubation was performed in the presence of a carbodiimide type agent soluble in water such as 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide at a final concentration of 0.3 M.

The derivatized oligonucleotide was then separated from the other agents and products using a standard technique for isolating oligonucleotides.

5   As discussed above, the mRNAs to be enriched may be treated to eliminate the 3' OH groups which may be present thereon. This may be accomplished by enzymatic ligation of sequences lacking a 3' OH, such as pCp, as described in Example 1. Alternatively, the 3' OH groups may be eliminated by alkaline hydrolysis as described in Example 8 below.

10   EXAMPLE 8

Elimination of 3' OH Groups of mRNA Using Alkaline Hydrolysis

In a total volume of 100 µl of 0.1 N sodium hydroxide, 1.5 µg mRNA is incubated for 40 to 60 minutes at 4°C. The solution is neutralized with acetic acid and precipitated with ethanol.

15   Following the optional elimination of the 3' OH groups, the diol groups at the 5' ends of the mRNAs are oxidized as described below in Example 9.

                                     EXAMPLE 9

Oxidation of Diols of mRNA

20   Up to 1 OD unit of RNA was dissolved in 9 µl of buffer (0.1 M sodium acetate, pH 6-7) or water and 3 µl of freshly prepared 0.1 M sodium periodate solution. The reaction was incubated for 1 h in the dark at 4°C or room temperature. Following the incubation, the reaction was stopped by adding 4 µl of 10% ethylene glycol. Thereafter the mixture was incubated at room temperature for 15 minutes. After ethanol precipitation, the product was

25   resuspended in at least 10 µl of water or appropriate buffer and dialyzed against water.

Following oxidation of the diol groups at the 5' ends of the mRNAs, the derivatized oligonucleotide was joined to the resulting aldehydes as described in Example 10.

30

EXAMPLE 10

Ligature of Aldehydes of mRNA to Derivatized Oligonucleotides

The oxidized mRNA was dissolved in an acidic medium such as 50 μl of sodium

acetate pH 4-6. Fifty μl of a solution of the derivatized oligonucleotide were added in order

5   to obtain an mRNA:derivatized oligonucleotide ratio of 1:20. The mixture was reduced with

a borohydride and incubated for 2 h at 37°C or overnight (14 h) at 10°C. The mixture was

then ethanol precipitated, resuspended in 10 μl or more of water or appropriate buffer and

dialyzed against distilled water. If desired, the resulting product may be analyzed using

acrylamide gel electrophoresis, HPLC analysis, or other conventional techniques.

10   Following the attachment of the derivatized oligonucleotide to the mRNAs, a reverse

transcription reaction may be performed as described in Example 11 below.

EXAMPLE 11

Reverse Transcription of mRNAs Ligatured to Derivatized Oligonucleotides

15   An oligodeoxyribonucleotide was derivatized as follows. Three OD units of an

oligodeoxyribonucleotide of sequence 5'ATCAAGAATTCGCACGAGACCATTA3' (SEQ

ID NO:3) having 5'-OH and 3'-P ends were dissolved in 70 μl of a 1.5 M

hydroxybenzotriazole solution, pH 5.3, prepared in dimethylformamide/water (75:25)

containing 2 μg of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide. The mixture was

20   incubated for 2 h 30 min at 22°C and then precipitated twice in LiClO₄/acetone. The pellet

was resuspended in 200 μl of 0.25 M hydrazine and incubated at 8°C from 3 to 14 h.

Following the hydrazine reaction, the mixture was precipitated twice in LiClO₄/acetone.

The messenger RNAs to be reverse transcribed were extracted from blocks of

placenta having sides of 2 cm which had been stored at -80°C. The total RNA was extracted

25   using conventional acidic phenol techniques. Oligo-dT chromatography was used to purify

the mRNAs. The integrity of the mRNAs was checked by Northern-blotting.

The diol groups on 7 μg of the placental mRNAs were oxidized as described above in

Example 9. The derivatized oligonucleotide was joined to the mRNAs as described in

Example 10 above except that the precipitation step was replaced by an exclusion

30   chromatography step to remove derivatized oligodeoxyribonucleotides which were not joined

to mRNAs. Exclusion chromatography was performed as follows:

Ten ml of Ultrogel AcA34 (BioSepra#230151) gel, a mix of agarose and acrylamide, were equilibrated in 50 ml of a solution of 10 mM Tris pH 8.0, 300 mM NaCl, 1 mM EDTA, and 0.05% SDS. The mixture was allowed to sediment. The supernatant was eliminated and the gel was resuspended in 50 ml of buffer. This procedure was repeated 2 or 3 times.

5   A glass bead (diameter 3 mm) was introduced into a 2 ml disposable pipette (length 25 cm). The pipette was filled with the gel suspension until the height of the gel stabilized at 1 cm from the top of the pipette. The column was then equilibrated with 20 ml of equilibration buffer (10 mM Tris HCl pH 7.4, 20 mM NaCl).

Ten μl of the mRNA which had reacted with the derivatized oligonucleotide were
10   mixed in 39 μl of 10 mM urea and 2 μl of blue-glycerol buffer, which had been prepared by dissolving 5 mg of bromophenol blue in 60% glycerol (v/v), and passing the mixture through a 0.45 μm diameter filter.

The column was then loaded with the mRNAs coupled to the oligonucleotide. As soon as the sample had penetrated, equilibration buffer was added. Hundred μl fractions were
15   then collected. Derivatized oligonucleotide which had not been attached to mRNA appeared in fraction 16 and later fractions. Thus, fractions 3 to 15 were combined and precipitated with ethanol.

To determine whether the derivatized oligonucleotide was actually linked to mRNA, one tenth of the combined fractions were spotted twice on a nylon membrane and hybridized
20   to a radioactive probe using conventional techniques. The ^{32}P labeled probe used in these hybridizations   was   an   oligodeoxyribonucleotide   of   sequence 5'TAATGGTCTCGTGCGAATTCTTGAT3' (SEQ ID NO:4) anticomplementary to the derivatized oligonucleotide. A signal observed after autoradiography, indicated that the derivatized oligonucleotide had been truly joined to the mRNA.

25   The remaining nine tenth of the mRNAs which had reacted with the derivatized oligonucleotide was reverse transcribed as follows. A reverse transcription reaction was carried out with reverse transcriptase following the manufacturer's instructions and 50 pmol of nonamers with random sequence as primers.

To ensure that reverse transcription had been carried out through the cap structure,
30   two types of experiments were performed.

In·the first approach, after elimination of RNA of the cDNA:RNA heteroduplexes obtained from the reverse transcription reaction by an alkaline hydrolysis, a portion of the resulting single stranded cDNAs was spotted on a positively charged membrane and hybridized, using conventional methods, to a ^{32}P labeled probe having a sequence identical to

5   that of the derivatized oligonucleotide. Control spots containing, 1 pmol, 100 fmol, 50 fmol, 10 fmol and 1 fmol of a control oligodeoxyribonucleotide of sequence identical to that of the derivatized oligonucleotide were included. The signal observed in the spots containing the cDNA indicated that approximately 15 fmol of the derivatized oligonucleotide had been reverse transcribed. These results demonstrate that the reverse transcription can be

10   performed through the cap and, in particular, that reverse transcriptase crosses the 5'-P-P-P-5' bond of the cap of eukaryotic messenger RNAs.

In the second type of experiment, the single stranded cDNAs obtained from the above first strand synthesis were used as template for PCR reactions. Two types of reactions were carried out. First, specific amplification of the mRNAs for alpha globin, dehydrogenase, pp15

15   and elongation factor E4 were carried out using the following pairs of oligodeoxyribonucleotide primers.

alpha-globin

GLO-S: 5'CCG ACA AGA CCA ACG TCA AGG CCG C3' (SEQ ID NO:5)

20   GLO-As: 5'TCA CCA GCA GGC AGT GGC TTA GGA G 3' (SEQ ID NO:6)

dehydrogenase

3 DH-S: 5'AGT GAT TCC TGC TAC TTT GGA TGG C3' (SEQ ID NO:7)

3 DH-As: 5'GCT TGG TCT TGT TCT GGA GTT TAG A3' (SEQ ID NO:8)

25

pp15

PP15-S: 5'TCC AGA ATG GGA GAC AAG CCA ATT T3' (SEQ ID NO:9)

PP15-As: 5'AGG GAG GAG GAA ACA GCG TGA GTC C3' (SEQ ID NO:10)

30   Elongation factor E4

EFA1-S: 5'ATG GGA AAG GAA AAG ACT CAT ATC A3' (SEQ ID NO:11)

EF1A-As: 5'AGC AGC AAC AAT CAG GAC AGC ACA G3' (SEQ ID NO:12)

Second, non specific amplifications were also carried out with the antisense oligodeoxyribonucleotides of the pairs described above and with a primer derived from the sequence of the derivatized oligodeoxyribonucleotide (5'ATCAAGAATTCGCACGAGACCATTA3') (SEQ ID NO:13).

One twentieth of the following RT-PCR product samples were run on a 1.5% agarose gel and stained with ethidium bromide.

Sample 1: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the presence of cDNA.

Sample 2: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the absence of added cDNA.

Sample 3: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the presence of cDNA.

Sample 4: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the absence of added cDNA.

Sample 5: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the presence of cDNA.

Sample 6: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the absence of added cDNA.

Sample 7: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the presence of added cDNA.

Sample 8: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the absence of added cDNA.

A band of the size expected for the PCR product was observed only in samples 1, 3, 5 and 7, thus indicating the presence of the corresponding sequence in the cDNA population.

PCR reactions were also carried out with the antisense oligonucleotides of the globin and dehydrogenase primers (SEQ ID NOs 6 and 8) and an oligonucleotide whose sequence corresponds to that of the derivatized oligonucleotide. The presence of PCR products of the expected size in the samples equivalent to above samples 1 and 3 indicated that the derivatized oligonucleotide had been linked to mRNA.

The above examples summarize the chemical procedure for enriching mRNAs for those having intact 5' ends as illustrated in Figure 1. Further detail regarding the chemical approaches for obtaining such mRNAs are disclosed in International Application No. WO96/34981, published November 7, 1996, which is incorporated herein by reference.

Strategies based on the above chemical modifications to the 5' cap structure may be utilized to generate cDNAs selected to include the 5' ends of the mRNAs from which they derived. In one version of such procedures, the 5' ends of the mRNAs are modified as described above. Thereafter, a reverse transcription reaction is conducted to extend a primer complementary to the 5' end of the mRNA. Single stranded RNAs are eliminated to obtain a population of cDNA/mRNA heteroduplexes in which the mRNA includes an intact 5' end. The resulting heteroduplexes may be captured on a solid phase coated with a molecule capable of interacting with the molecule used to derivatize the 5' end of the mRNA. Thereafter, the strands of the heteroduplexes are separated to recover single stranded first cDNA strands which include the 5' end of the mRNA. Second strand cDNA synthesis may then proceed using conventional techniques. For example, the procedures disclosed in WO 96/34981 or in Carninci. et al., *Genomics* 37:327-336, 1996, the disclosures of which are incorporated herein by reference, may be employed to select cDNAs which include the sequence derived from the 5' end of the coding sequence of the mRNA.

Following ligation of the oligonucleotide tag to the 5' cap of the mRNA, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Following elimination of the RNA component of the resulting heteroduplex using standard techniques, second strand cDNA synthesis is conducted with a primer complementary to the oligonucleotide tag.

2. Enzymatic Methods for Obtaining mRNAs having Intact 5' Ends

Other techniques for selecting cDNAs extending to the 5' end of the mRNA from which they are derived are fully enzymatic. Some versions of these techniques are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato *et al.*, *Gene* 150:243-250, 1994, the disclosures of which are incorporated herein by reference.

Briefly, in such approaches, isolated mRNA is treated with alkaline phosphatase to remove the phosphate groups present on the 5' ends of uncapped incomplete mRNAs. Following this procedure, the cap present on full length mRNAs is enzymatically removed with a decapping enzyme such as T4 polynucleotide kinase or tobacco acid pyrophosphatase.

5   An oligonucleotide, which may be either a DNA oligonucleotide or a DNA-RNA hybrid oligonucleotide having RNA at its 3' end, is then ligated to the phosphate present at the 5' end of the decapped mRNA using T4 RNA ligase. The oligonucleotide may include a restriction site to facilitate cloning of the cDNAs following their synthesis. Example 12 below describes one enzymatic method based on the doctoral thesis of Dumas.

10

EXAMPLE 12

Enzymatic Approach for Obtaining 5' ESTs

Twenty micrograms of PolyA+ RNA were dephosphorylated using Calf Intestinal Phosphatase (Biolabs). After a phenol chloroform extraction, the cap structure of mRNA

15   was hydrolysed using the Tobacco Acid Pyrophosphatase (purified as described by Shinshi *et al.*, *Biochemistry* 15: 2185-2190, 1976) and a hemi 5'DNA/RNA-3' oligonucleotide having an unphosphorylated 5' end, a stretch of adenosine ribophosphate at the 3' end, and an EcoRI site near the 5' end was ligated to the 5'P ends of mRNA using the T4 RNA ligase (Biolabs). Oligonucleotides suitable for use in this procedure are preferably 30 to 50 bases in length.

20   Oligonucleotides having an unphosphorylated 5' end may be synthesized by adding a fluorochrome at the 5' end. The inclusion of a stretch of adenosine ribophosphates at the 3' end of the oligonucleotide increases ligation efficiency. It will be appreciated that the oligonucleotide may contain cloning sites other than EcoRI.

Following ligation of the oligonucleotide to the phosphate present at the 5' end of the

25   decapped mRNA, first and second strand cDNA synthesis is carried out using conventional methods or those specified in EPO 625,572 and Kato *et al. supra*, and Dumas Milne Edwards, *supra*, the disclosures of which are incorporated herein by reference. The resulting cDNA may then be ligated into vectors such as those disclosed in Kato *et al.*, *supra* or other nucleic acid vectors known to those skilled in the art using techniques such as those described

30   in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated herein by reference.

II. Obtention and Characterization of the 5' ESTs of the Present Invention

The 5' ESTs of the present invention were obtained using the aforementioned chemical and enzymatic approaches for enriching mRNAs for those having intact 5' ends as decribed below.

1. Obtention of 5' ESTS Using mRNAs with Intact 5' Ends

First, mRNAs were prepared as described in Example 13 below.

EXAMPLE 13

Preparation of mRNA With Intact 5' Ends

Total human RNAs or polyA$^+$ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as follows. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczyniski and Sacchi, *Analytical Biochemistry* 162:156-159, 1987). PolyA$^+$ RNA was isolated from total RNA (LABIMO) by two passes of oligo dT chromatography, as described by Aviv and Leder, *Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972 in order to eliminate ribosomal RNA.

The quality and the integrity of the polyA+ RNAs were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the polyA$^+$ mRNAs by ribosomal sequences was checked using Northern blots and a probe derived from the sequence of the 28S rRNA. Preparations of mRNAs with less than 5% of rRNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed fungal mRNAs was examined using PCR.

Following preparation of the mRNAs, the above described chemical and/or the enzymatic procedures for enriching mRNAs for thoses having intact 5' ends were employed to obtain 5' ESTs from various tissues. In both approaches, an oligonucleotide tag was attached to the 5' ends of the mRNAs. The oligonucleotide tag had an EcoRI site therein to facilitate later cloning procedures. To facilitate the processing of single stranded and double stranded cDNA obtained in the construction of the librairies, the same nucleotidic sequence

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was used to design the ligated oligonucleotide in both chemical and enzymatic approaches. Nevertheless, in the chemical procedure, the tag used was an oligodeoxyribonucleotide which was linked to the cap of the mRNA whereas in the enzymatic ligation, the tag was a chimeric hemi 5'DNA/RNA3' oligonucleotide which was ligated to the 5' end of decapped mRNA as described in example 12.

Following attachment of the oligonucleotide tag to the mRNA by either the chemical or enzymatic methods, the integrity of the mRNA was examined by performing a Northern blot with 200 to 500 ng of mRNA using a probe complementary to the oligonucleotide tag before performing the first strand synthesis as described in example 14.

EXAMPLE 14

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

For the mRNAs joined to oligonucleotide tags using both the chemical and enzymatic methods, first strand cDNA synthesis was performed using the Superscript II (Gibco BRL) or the Rnase H Minus M-MLV (Promega) reverse transcriptase with random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of RNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

For both the chemical and the enzymatic methods, the second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5' end of the ligated oligonucleotide described in Example 12. Preferably, the primer is 20-25 bases in length. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following cDNA synthesis, the cDNAs were cloned into pBlueScript as described in Example 15 below.

EXAMPLE 15

Cloning of cDNAsderived from mRNA with intact 5' ends into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was

used during cDNA synthesis, the EcoRI site present in the tag was the only hemi-methylated site, hence the only site susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra) and fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned

5   into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached were then selected as described in Example 16 below.

10

EXAMPLE 16

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows.

15   Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, 13: 124-131, 1992. In this procedure, the single stranded DNA was

20   hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide described in Example 13. Preferably, the primer has a length of 20-25 bases. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the

25   magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. Alternatively, protocoles such as the one described in the Gene Trapper kit available from Gibco BRL may be used. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated to typically rank between 90

30   and 98% using dot blot analysis.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP).
A copy of the MTP was stored for future needs. Then the libraries were transferred into 96
MTP and sequenced as described below.

5   **EXAMPLE 17**
                    Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE 9600 thermocyclers (Perkin-Elmer,
Applied Biosystems Division, Foster City, CA), using standard SETA-A and SETA-B
primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling
10   conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers
(Perkin Elmer). Sequencing reactions were performed using PE 9600 thermocyclers with
standard dye-primer chemistry and ThermoSequenase (Amersham Pharmacia Biotech). The
primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The
15   primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs
used in the sequencing reactions were purchased from Boehringer. Sequencing buffer,
reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with ethanol,
resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel.
20   Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and
the sequence data were collected and analyzed using the ABI Prism DNA Sequencing
Analysis Software, version 2.1.2.

2. Computer analysis of the Obtained 5' ESTs: Construction of NetGene and SignalTag
25   databases

The sequence data from the 44 cDNA libraries made as described above were
transferred to a proprietary database, where quality control and validation steps were
performed. A proprietary base-caller, working using a Unix system, automatically flagged
suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the
30   noise level. The proprietary base-caller also performed an automatic trimming. Any stretch
of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was

discarded. · Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case to case basis.

Following sequencing as described above, the sequences of the 5' ESTs were entered in NetGene™, a proprietary database called for storage and manipulation as described below. It will be appreciated by those skilled in the art that the data could be stored and manipulated on any medium which can be read and accessed by a computer. Computer readable media include magnetically, optically, or electronically readable media. For example, the computer readable media may be a hard disc, a floppy disc, a magnetic tape, CD-ROM, RAM, or ROM as well as other types of other media known to those skilled in the art.

In addition, the sequence data may be stored and manipulated in a variety of data processor programs in a diversity of formats. For instance, the sequence data may be stored as text in a word processing file, such as Microsoft WORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE.

The computer readable media on which the sequence information is stored may be in a personal computer, a network, a server or other computer systems known to those skilled in the art. The computer or other system preferably includes the storage media described above, and a processor for accessing and manipulating the sequence data. Once the sequence data has been stored, it may be manipulated and searched to locate those stored sequences which contain a desired nucleic acid sequence or which encode a protein having a particular functional domain. For example, the stored sequence information may be compared to other known sequences to identify homologies, motifs implicated in biological function, or structural motifs.

Programs which may be used to search or compare the stored sequences include the MacPattern (EMBL), BLAST, and BLAST2 program series (NCBI), basic local alignment search tool programs for nucleotide (BLASTN) and peptide (BLASTX) comparisons (Altschul et al, J. Mol. Biol. 215: 403, 1990) and FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85: 2444, 1988). The BLAST programs then extend the alignments on the basis of defined match and mismatch criteria.

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Motifs which may be detected using the above programs and those described in Example 28 include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

Before searching the cDNAs in the NetGene™ database for sequence motifs of interest, cDNAs derived from mRNAs which were not of interest were identified and eliminated from further consideration as described in Example 18 below.

EXAMPLE 18

Elimination of Undesired Sequences from Further Consideration

5' ESTs in the NetGene™ database which were derived from undesired sequences such as transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs, fungal RNAs, Alu sequences, L1 sequences, or repeat sequences were identified using the FASTA and BLASTN programs with the parameters listed in Table I.

To eliminate 5' ESTs encoding tRNAs from further consideration, the 5' EST sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. The comparison was performed using FASTA on both strands of the 5' ESTs. Sequences having more than 80% homology over more than 60 nucleotides were identified as tRNA. Of the 144,341 sequences screened, 26 were identified as tRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding rRNAs from further consideration, the 5' EST sequences were compared to the sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as rRNAs. Of the 144,341 sequences screened, 3,312 were identified as rRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding mtRNAs from further consideration, the 5' EST sequences were compared to the sequences of the two known mitochondrial genomes for

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which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40

5   nucleotides were identified as mtRNAs. Of the 144,341 sequences screened, 6,110 were identified as mtRNAs and eliminated from further consideration.

Sequences which might have resulted from exogenous contaminants were eliminated from further consideration by comparing the 5' EST sequences to release 46 of the EMBL bacterial and fungal divisions using BLASTN with the parameter S=144. All sequences

10   having more than 90% homology over at least 40 nucleotides were identified as exogenous contaminants. Of the 42 cDNA libraries examined, the average percentages of prokaryotic and fungal sequences contained therein were 0.2% and 0.5% respectively. Among these sequences, only one could be identified as a sequence specific to fungi. The others were either fungal or prokaryotic sequences having homologies with vertebrate sequences or

15   including repeat sequences which had not been masked during the electronic comparison.

In addition, the 5' ESTs were compared to 6093 Alu sequences and 1115 L1 sequences to mask 5' ESTs containing such repeat sequences. 5' ESTs including THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats were also eliminated from further consideration. On average, 11.5% of the sequences in the libraries

20   contained repeat sequences. Of this 11.5%, 7% contained Alu repeats, 3.3% contained L1 repeats and the remaining 1.2% were derived from the other screened types of repetitive sequences. These percentages are consistent with those found in cDNA libraries prepared by other groups. For example, the cDNA libraries of Adams *et al.* contained between 0% and 7.4% Alu repeats depending on the source of the RNA which was used to prepare the cDNA

25   library (Adams *et al.*, *Nature* 377:174, 1996).

The sequences of those 5' ESTs remaining after the elimination of undesirable sequences were compared with the sequences of known human mRNAs to determine the accuracy of the sequencing procedures described above.

30

EXAMPLE 19

Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described above, the sequences of 5' ESTs derived from known sequences were identified and compared to the original known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database. The 6655 5' ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy.

This analysis revealed that the sequences incorporated in the NetGene™ database had an accuracy of more than 99.5%.

To determine the efficiency with which the above selection procedures select cDNAs which include the 5' ends of their corresponding mRNAs, the following analysis was performed.

EXAMPLE 20

Determination of Efficiency of 5' EST Selection

To determine the efficiency at which the above selection procedures isolated 5' ESTs which included sequences close to the 5' end of the mRNAs from which they derived, the sequences of the ends of the 5' ESTs derived from the elongation factor 1 subunit α and ferritin heavy chain genes were compared to the known cDNA sequences of these genes. Since the transcription start sites of both genes are well characterized, they may be used to determine the percentage of derived 5' ESTs which included the authentic transcription start sites.

For both genes, more than 95% of the obtained 5' ESTs actually included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the NetGene™ database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for

comparison. The 5' ends of more than 85% of 5' ESTs derived from mRNAs included in the GeneBank database were located close to the 5' ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends of their corresponding mRNAs.

The EST libraries made above included multiple 5' ESTs derived from the same mRNA. The sequences of such 5' ESTs were compared to one another and the longest 5' ESTs for each mRNA were identified. Overlapping cDNAs were assembled into continuous sequences (contigs). The resulting continuous sequences were then compared to public databases to gauge their similarity to known sequences, as described in Example 21 below.

EXAMPLE 21

Clustering of the 5' ESTs and Calculation of Novelty Indices for cDNA Libraries

For each sequenced EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others with BLASTN2 (direct strand, parameters S=107). ESTs with High Scoring Segment Pairs (HSPs) at least 25 bp long, having 95% identical bases and beginning closer than 10 bp from each EST 5' end were grouped. The longest sequence found in the cluster was used as representative of the group. A global clustering between libraries was then performed leading to the definition of super-contigs.

To assess the yield of new sequences within the EST libraries, a novelty rate (NR) was defined as: NR= 100 X (Number of new unique sequences found in the library/Total number of sequences from the library). Typically, novelty rating ranged between 10% and 41% depending on the tissue from which the EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

Following characterization as described above, the collection of 5' ESTs in NetGene™ was screened to identify those 5' ESTs bearing potential signal sequences as described in Example 22 below.

35

EXAMPLE 22

Identification of Potential Signal Sequences in 5' ESTs

The 5' ESTs in the NetGene™ database were screened to identify those having an uninterrupted open reading frame (ORF) longer than 45 nucleotides beginning with an ATG

5   codon and extending to the end of the EST. Approximately half of the cDNA sequences in NetGene™ contained such an ORF. The ORFs of these 5' ESTs were then searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, *Nucleic Acids Res.* 14:4683-4690, 1986, the disclosure of which is incorporated herein by reference. Those 5' EST sequences encoding a stretch of at least 15 amino acid

10   long with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those 5' ESTs which matched a known human mRNA or EST sequence and had a 5' end more than 20 nucleotides downstream of the known 5' end were excluded from further analysis. The remaining cDNAs having signal sequences therein were included in a database called SignalTag™.

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To confirm the accuracy of the above method for identifying signal sequences, the analysis of Example 23 was performed.

EXAMPLE 23

20   ### Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino acids located at the N terminus of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a

25   non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was

30   calculated based on either the assumption that 10% of human proteins are secreted or the

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assumption that 20% of human proteins arc secreted. The results of this analysis are shown in Figure 2 and in Table IV.

Using the above method of identification of secretory proteins, 5' ESTs of the following polypeptides known to be secreted were obtained: human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Such vectors are designed to confer the ability to grow in selective medium only to host cells containing a vector with an operably linked signal sequence. For example, to confirm that a 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637, the disclosure of which is incorporated herein by reference. Growth of host cells containing signal sequence selection vectors with the correctly inserted 5' EST signal sequence confirms that the 5' EST encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs into expression vectors such as pXT1 (as described below in example 30), or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from control cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

Those 5' ESTs which encoded a signal peptide, as determined by the method of Example 22 above, were further grouped into four categories based on their homology to known sequences as described in Example 24 below.

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EXAMPLE 24

Categorization of 5' ESTs Encoding a Signal Peptide

Those 5' ESTs having a sequence not matching any known vertebrate sequence nor any publicly available EST sequence were designated "new." Of the sequences in the SignalTag™ database, 947 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs having a sequence not matching any vertebrate sequence but matching a publicly known EST were designated "EST-ext", provided that the known EST sequence was extended by at least 40 nucleotides in the 5' direction. Of the sequences in the SignalTag™ database, 150 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those ESTs not matching any vertebrate sequence but matching a publicly known EST without extending the known EST by at least 40 nucleotides in the 5' direction were designated "EST." Of the sequences in the SignalTag™ database, 599 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs matching a human mRNA sequence but extending the known sequence by at least 40 nucleotides in the 5' direction were designated "VERT-ext." Of the sequences in the SignalTag™ database, 23 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category. Included in this category was a 5' EST which extended the known sequence of the human translocase mRNA by more than 200 bases in the 5' direction. A 5' EST which extended the sequence of a human tumor suppressor gene in the 5' direction was also identified.

Table V shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

3. Evaluation of Spatial and Temporal Expression of mRNAs Corresponding to the 5'ESTs or Extended cDNAs

Each of the 5' ESTs was also categorized based on the tissue from which its corresponding mRNA was obtained, as described below in Example 25.

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EXAMPLE 25

Categorization of Expression Patterns

Table VI shows the distribution of 5' ESTs in each of the above defined category with respect to the tissue from which the 5'ESTs of the corresponding mRNA were obtained.

5   Table II provides the sequence identification numbers of 5' EST sequences derived from brain, the categories in which these sequences fall, and the von Heijne's score of the signal peptides which they encode. The 5' EST sequences and the amino acid sequences they encode are provided in the appended sequence listings. Table III provides the sequence ID numbers of the 5' ESTs and the sequences of the signal peptides which they encode. The

10   sequences of the 5' ESTs and the polypeptides they encode are provided in the sequence listing appended hereto.

The sequences of DNA SEQ ID NOs: 38-270 can readily be screened for any errors therein and any sequence ambiguities can be resolved by resequencing a fragment containing such errors or amibiguities on both strands. Such fragments may be obtained from the

15   plasmids stored in the inventors' laboratory or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the amibiguity or error. Upon resolution of an error or ambiguity, the corresponding corrections can be made

20   in the protein sequences encoded by the DNA containing the error or amibiguity.

In addition to categorizing the 5' ESTs with respect to their tissue of origin, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs, as well as their expression levels, may be determined as described in Example 26 below. Characterization of the spatial and temporal expression patterns and expression levels of these

25   mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

Furthermore, 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from the lack of

30   expression, over expression, or under expression of an mRNA corresponding to a 5' EST. By comparing mRNA expression patterns and quantities in samples taken from healthy

individuals with those from individuals suffering from a particular disease, 5' ESTs responsible for the disease may be identified.

5   It will be appreciated that the results of the above characterization procedures for 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs. It will also be appreciated that if desired, characterization may be delayed until extended cDNAs have been obtained rather than characterizing the ESTs themselves.

10   EXAMPLE 26

Evaluation of Expression Levels and Patterns of mRNAs

Corresponding to 5' ESTs or Extended cDNAs

Expression levels and patterns of mRNAs corresponding to 5' ESTs or extended cDNAs (obtainable as described below in example 27) may be analyzed by solution
15   hybridization with long probes as described in International Patent Application No. WO 97/05277, the entire contents of which are hereby incorporated by reference. Briefly, a 5' EST, extended cDNA, or fragment thereof corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3, T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the 5' EST or
20   extended cDNA has 100 or more nucleotides. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (i.e. biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The
25   unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (i.e. RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

30   The 5' ESTs, extended cDNAs, or fragments thereof may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK

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Patent Application No. 2 305 241 A, the entire contents of which are incorporated by reference. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which gene expression patterns must be determined. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction

5   endonuclease, called an anchoring enzyme, having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a so-called tagging endonuclease is

10   ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short tag fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the tagging

15   endonuclease to generate short tag fragments derived from the cDNAs in the second pool. The tags resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce so-called ditags. In some embodiments, the ditags are concatamerized to produce ligation products containing from 2 to 200 ditags. The tag sequences are then determined and compared to the sequences of the

20   5' ESTs or extended cDNAs to determine which 5' ESTs or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used

25   herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of full length cDNAs (*i.e.* extended cDNAs which include the coding sequence for the signal peptide, the coding sequence for the mature protein, and a stop codon), extended cDNAs, 5' ESTs or fragments thereof of sufficient length to permit specific detection of gene expression. Preferably, the fragments are at least 15 nucleotides in length.

30   More preferably, the fragments are at least 100 nucleotide long. More preferably, the

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fragments are more than 100 nucleotides in length. In some embodiments, the fragments may be more than 500 nucleotide long.

For example, quantitative analysis of gene expression may be performed with full length cDNAs as defined below, extended cDNAs, 5' ESTs, or fragments thereof in a complementary DNA microarray as described by Schena *et al.* (*Science* 270:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619, 1996). Full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm^2 microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in complementary DNA arrays as described by Pietu *et al.*. (*Genome Research* 6:492-503, 1996). The full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the 5' ESTs or extended cDNAs can be done through high density nucleotide arrays as described by Lockhart *et al.* (*Nature Biotechnology*

14: 1675-1680, 1996) and Sosnowsky *et al.* (*Proc. Natl. Acad. Sci.* 94:1119-1123, 1997). Oligonucleotides of 15-50 nucleotides corresponding to sequences of the 5' ESTs or extended cDNAs are synthesized directly on the chip (Lockhart *et al.*, *supra*) or synthesized and then addressed to the chip (Sosnowsky *et al.*, *supra*). Preferably, the oligonucleotides

5   are about 20 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart *et al*, *supra* and application of different

10   electric fields (Sonowsky et *al*, *supra.*), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

15

III. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended

20   cDNAs which contain sequences adjacent to the 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site, the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide. Such extended cDNAs are referred to herein as "full length cDNAs." Alternatively, the extended cDNAs may include only the

25   sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Example 27 below describes a general method for obtaining extended cDNAs using 5' ESTs. Example 28 below provides experimental results, using the method explained in example 27, describing several extended cDNAs including the entire coding sequence and

30   authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 27, 28, and 29 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of the secreted proteins encoded by the genes corresponding to the 5' ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 10 amino acids of one of the proteins encoded by the sequences of SEQ ID NOs: 38-270. In further embodiments, the extended cDNAs encode at least 20 amino acids of the proteins encoded by the sequences of SEQ ID NOs: 38-270. In further embodiments, the extended cDNAs encode at least 30 amino amino acids of the sequences of SEQ ID NOs: 38-270. In a preferred embodiment, the extended cDNAs encode a full length protein sequence, which includes the protein coding sequences of SEQ ID NOs: 38-270.

EXAMPLE 27

General Method for Using 5' ESTs to Clone and Sequence cDNAs which Include the Entire Coding Region and the Authentic 5' End of the Corresponding mRNA

The following general method has been used to quickly and efficiently isolate extended cDNAs having the authentic 5' ends of their corresponding mRNAs as well as the full protein coding sequence and including sequence adjacent to the sequences of the 5' ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST in the NetGene™ database, including those 5' ESTs encoding polypeptides belonging to secreted proteins. The method is summarized in figure 3.

1. Obtention of Extended cDNAs

a) First strand synthesis

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly 14dT primer containing a 49 nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of the mRNA. For example, the primer may have the following sequence: 5'-ATC GTT GAG ACT CGT ACC AGC AGA GTC ACG AGA GAG ACT ACA CGG TAC TGG TTT TTT TTT TTT TTVN -3' (SEQ ID NO:14). Those skilled in the art will appreciate that other sequences may also be added to the poly dT sequence and used to prime the first strand synthesis. Using this primer and a reverse

transcriptase such as the Superscript II (Gibco BRL) or Rnase H Minus M-MLV (Promega) enzyme, a reverse transcript anchored at the 3' polyA site of the RNAs is generated.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer are

5   eliminated with an exclusion column such as an AcA34 (Biosepra) matrix as explained in Example 11.

b) Second strand synthesis

A pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST and the known 3' end added by the poly dT primer used in the first strand

10   synthesis. Softwares used to design primers are either based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais *et al., Nucleic Acids Res.* **19**: 3887-3891, 1991) such as PC-Rare (http://bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html).

15   Preferably, the nested primers at the 5' end are separated from one another by four to nine bases. The 5' primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

Preferably, the nested primers at the 3' end are separated from one another by four to nine bases. For example, the nested 3' primers may have the following sequences: (5'- CCA

20   GCA GAG TCA CGA GAG AGA CTA CAC GG -3'(SEQ ID NO:15), and 5'- CAC GAG AGA GAC TAC ACG GTA CTG G -3' (SEQ ID NO:16). These primers were selected because they have melting temperatures and specificities compatible with their use in PCR. However, those skilled in the art will appreciate that other sequences may also be used as primers.

25   The first PCR run of 25 cycles is performed using the Advantage Tth Polymerase Mix (Clontech) and the outer primer from each of the nested pairs. A second 20 cycle PCR using the same enzyme and the inner primer from each of the nested pairs is then performed on 1/2500 of the first PCR product. Thereafter, the primers and nucleotides are removed.

30

2. Sequencing of Full Length Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon

5   thus yielding a nested PCR product containing the whole coding sequence. Such a full length extended cDNA undergoes a direct cloning procedure as described in section a. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b.

10   *a) Nested PCR products containing complete ORFs*

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST sequence, it is cloned in an appropriate vector such as pED6dpc2, as described in section 3.

b) Nested PCR products containing incomplete ORFs

15   When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products as described in the following section.

20   Once the full coding sequence has been completely determined, new primers compatible for PCR use are designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, *i.e.* the polyA tract and sometimes the polyadenylation signal, as illustrated in

25   figure 3. Such full length extended cDNAs are then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs is performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

30   In order to sequence PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton *et*

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al., Genome Science Technol. 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag using minimum overlaps of 32 nucleotides. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment is assessed as follows. Since sequences located after a polyA tract are difficult to determine precisely in the case of uncloned products, sequencing and primer walking processes for PCR products are interrupted when a polyA tract is identified in extended cDNAs obtained as described in case b. The sequence length is compared to the size of the nested PCR product obtained as described above. Due to the limited accuracy of the determination of the PCR product size by gel electrophoresis, a sequence is considered complete if the size of the obtained sequence is at least 70 % the size of the first nested PCR product. If the length of the sequence determined from the computer analysis is not at least 70% of the length of the nested PCR product, these PCR products are cloned and the sequence of the insertion is determined. When Northern blot data are available, the size of the mRNA detected for a given PCR product is used to finally assess that the sequence is complete. Sequences which do not fulfill the above criteria are discarded and will undergo a new isolation procedure.

Sequence data of all extended cDNAs are then transferred to a proprietary database, where quality controls and validation steps are carried out as described in example 15.

3. Cloning of Full Length Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into the expression vector pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA) as follows. pED6dpc2 vector DNA is prepared with blunt ends by performing an EcoRI digestion followed by a fill in reaction. The blunt ended vector is dephosphorylated. After removal of PCR primers and ethanol precipitation, the PCR product containing the full coding sequence or the extended cDNA obtained as described above is phosphorylated with a kinase subsequently removed by phenol-Sevag extraction and precipitation. The double stranded extended cDNA is then ligated to the vector and the resulting expression plasmid introduced into appropriate host cells.

47

Since the PCR products obtained as described above are blunt ended molecules that can be cloned in either direction, the orientation of several clones for each PCR product is determined. Then, 4 to 10 clones are ordered in microtiter plates and subjected to a PCR reaction using a first primer located in the vector close to the cloning site and a second primer located in the portion of the extended cDNA corresponding to the 3' end of the mRNA. This second primer may be the antisense primer used in anchored PCR in the case of direct cloning (case a) or the antisense primer located inside the 3'UTR in the case of indirect cloning (case b). Clones in which the start codon of the extended cDNA is operably linked to the promoter in the vector so as to permit expression of the protein encoded by the extended cDNA are conserved and sequenced. In addition to the ends of cDNA inserts, approximately 50 bp of vector DNA on each side of the cDNA insert are also sequenced.

The cloned PCR products are then entirely sequenced according to the aforementioned procedure. In this case, contigation of long fragments is then performed on walking sequences that have already contigated for uncloned PCR products during primer walking. Sequencing of cloned amplicons is complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends.

4. Computer analysis of Full Length Extended cDNA

Sequences of all full length extended cDNAs are then submitted to further analysis as described below. Before searching the extended full length cDNAs for sequences of interest, extended cDNAs which are not of interest (vector RNAs, transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs and fungal RNAs) are discarded using methods essentially similar to those described for 5'ESTs in Example 18.

a) Identification of structural features

Structural features, e.g. polyA tail and polyadenylation signal, of the sequences of full length extended cDNAs are subsequently determined as follows.

A polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 100 nt of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not

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readable after such a polyA stretch. Stretches having more than 90% homology over 8 nucleotides are identified as polyA tails using BLAST2N.

To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 bp preceding the polyA tail are first searched for the canonic polyadenylation AAUAAA signal and, if the canonic signal is not detected, for the alternative AUUAAA signal (Sheets *et al.*, *Nuc. Acids Res.* 18: 5799-5805, 1990). If neither of these consensus polyadenylation signals is found, the canonic motif is searched again allowing one mismatch to account for possible sequencing errors. More than 85 % of identified polyadenylation signals of either type actually ends 10 to 30 bp from the polyA tail. Alternative AUUAAA signals represents approximately 15 % of the total number of identified polyadenylation signals.

b) Identification of functional features

Functional features, e.g. ORFs and signal sequences, of the sequences of full length extended cDNAs were subsequently determined as follows.

The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation intiation codon and ending with a stop codon. ORFs encoding at least 20 amino acids are preferred.

Each found ORF is then scanned for the presence of a signal peptide in the first 50 amino-acids or, where appropriate, within shorter regions down to 20 amino acids or less in the ORF, using the matrix method of von Heijne (*Nuc. Acids Res.* 14: 4683-4690, 1986), the disclosure of which is incorporated herein by reference as described in Example 22.

c) Homology to either nucleotidic or proteic sequences

Categorization of full-length sequences may be achieved using procedures essentially similar to those described for 5'ESTs in Example 24.

Extended cDNAs prepared as described above may be subsequently engineered to obtain nucleic acids which include desired portions of the extended cDNA using conventional techniques such as subcloning, PCR, or *in vitro* oligonucleotide synthesis. For example, nucleic acids which include only the full coding sequences (*i.e.* the sequences encoding the signal peptide and the mature protein remaining after the signal peptide is cleaved off) may be

obtained using techniques known to those skilled in the art. Alternatively, conventional techniques may be applied to obtain nucleic acids which contain only the coding sequences for the mature protein remaining after the signal peptide is cleaved off or nucleic acids which contain only the coding sequences for the signal peptides.

5   Similarly, nucleic acids containing any other desired portion of the coding sequences for the secreted protein may be obtained. For example, the nucleic acid may contain at least 10 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 15 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. Alternatively, the

10   nucleic acid may contain at least 20 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 25 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In yet another embodiment, the nucleic acid may contain at least 40 consecutive bases of an extended cDNA such as one of the extended cDNAs described

15   below.

Once an extended cDNA has been obtained, it can be sequenced to determine the amino acid sequence it encodes. Once the encoded amino acid sequence has been determined, one can create and identify any of the many conceivable cDNAs that will encode that protein by simply using the degeneracy of the genetic code. For example, allelic variants

20   or other homologous nucleic acids can be identified as described below. Alternatively, nucleic acids encoding the desired amino acid sequence can be synthesized *in vitro*.

In a preferred embodiment, the coding sequence may be selected using the known codon or codon pair preferences for the host organism in which the cDNA is to be expressed.

The extended cDNAs derived from the 5' ESTS of the present invention were

25   obtained as described in Example 28 below.

EXAMPLE 28

Characterization of cloned extended cDNAs obtained using 5' ESTs

The procedure described in Example 27 above was used to obtain the extended

30   cDNAs derived from the 5' ESTs of the present invention in a variety of tissues. The following list provides a few examples of thus obtained extended cDNAs.

Using this approach, the full length cDNA of SEQ ID NO:17 (internal identification number 48-19-3-G1-FL1) was obtained. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MKKVLLLITAILAVAVG (SEQ ID NO: 18) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:19 (internal identification number 58-34-2-E7-FL2) was also obtained using this procedure. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MWWFQQGLSFLPSALVIWTSA (SEQ ID NO:20) having a von Heijne score of 5.5.

Another full length cDNA obtained using the procedure described above has the sequence of SEQ ID NO:21 (internal identification number 51-27-1-E8-FL1). This cDNA, falls into the "EST-ext" category described above and encodes the signal peptide MVLTTLPSANSANSPVNMPTTGPNSLSYASSALSPCLT (SEQ ID NO:22) having a von Heijne score of 5.9.

The above procedure was also used to obtain a full length cDNA having the sequence of SEQ ID NO:23 (internal identification number 76-4-1-G5-FL1). This cDNA falls into the "EST-ext" category described above and encodes the signal peptide ILSTVTALTFAXA (SEQ ID NO:24) having a von Heijne score of 5.5.

The full length cDNA of SEQ ID NO:25 (internal identification number 51-3-3-B10-FL3) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LVLTLCTLPLAVA (SEQ ID NO:26) having a von Heijne score of 10.1.

The full length cDNA of SEQ ID NO:27 (internal identification number 58-35-2-F10-FL2) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:28) having a von Heijne score of 10.7.

Bacterial clones containing plasmids containing the full length cDNAs described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the stored materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired

the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the cDNA insertion. The PCR product which corresponds to the cDNA can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The polypeptides encoded by the extended cDNAs may be screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The conserved regions have been used to derive consensus patterns or matrices included in the PROSITE data bank, in particular in the file prosite.dat (Release 13.0 of November 1995, located at http://expasy.hcuge.ch/sprot/prosite.html. Prosite_convert and prosite_scan programs (http://ulrec3.unil.ch/ftpserveur/prosite_scan) may be used to find signatures on the extended cDNAs.

For each pattern obtained with the prosite_convert program from the prosite.dat file, the accuracy of the detection on a new protein sequence may be assessed by evaluating the frequency of irrelevant hits on the population of human secreted proteins included in the data bank SWISSPROT. The ratio between the number of hits on shuffled proteins (with a window size of 20 amino acids) and the number of hits on native (unshuffled) proteins may be used as an index. Every pattern for which the ratio is greater than 20% (one hit on shuffled proteins for 5 hits on native proteins) may be skipped during the search with prosite_scan. The program used to shuffle protein sequences (db_shuffled) and the program used to determine the statistics for each pattern in the protein data banks (prosite_statistics) are available on the ftp site http://ulrec3.unil.ch/ftpserveur/prosite_scan.

In addition to PCR based methods for obtaining extended cDNAs, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs or 5' ESTs. Example 29 below provides examples of such methods.

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EXAMPLE 29

Methods for Obtaining cDNAs which include the Entire Coding Region and the Authentic

5'End of the Corresponding mRNA

A full length cDNA library can be made using the strategies described in Examples

13, 14, 15, and 16 above by replacing the random nonamer used in Example 14 with an oligo-

dT primer. For instance, the oligonucleotide of SEQ ID NO:14 may be used.

Alternatively, a cDNA library or genomic DNA library may be obtained from a

commercial source or made using techniques familiar to those skilled in the art. Such cDNA

or genomic DNA libraries may be used to isolate extended cDNAs obtained from 5' EST or

nucleic acids homologous to extended cDNAs or 5' EST as follows. The cDNA library or

genomic DNA library is hybridized to a detectable probe comprising at least 10 consecutive

nucleotides from the 5' EST or extended cDNA using conventional techniques. Preferably,

the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or

extended cDNA. More preferably, the probe comprises at least 20 to 30 consecutive

nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises

more than 30 nucleotides from the 5' EST or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given

probe sequence are disclosed in Sambrook et al., Molecular Cloning: A Laboratory Manual

2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated

herein by reference. The same techniques may be used to isolate genomic DNAs.

Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are

identified and isolated for further manipulation as follows. A probe comprising at least 10

consecutive nucleotides from the 5' EST or extended cDNA is labeled with a detectable label

such as a radioisotope or a fluorescent molecule. Preferably, the probe comprises at least 12,

15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the

probe comprises 20 to 30 consecutive nucleotides from the 5' EST or extended cDNA. In

some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or

extended cDNA.

Techniques for labeling the probe are well known and include phosphorylation with

polynucleotide kinase, nick translation, in vitro transcription, and non radioactive techniques.

The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter

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and denatured. After blocking of non specific sites, the filter is incubated with the labeled probe for an amount of time sufficient to allow binding of the probe to cDNAs or genomic DNAs containing a sequence capable of hybridizing thereto.

By varying the stringency of the hybridization conditions used to identify extended cDNAs or genomic DNAs which hybridize to the detectable probe, extended cDNAS having different levels of homology to the probe can be identified and isolated as described below.

1. Identification of Extended cDNA or Genomic cDNA Sequences Having a High Degree of Homology to the Labeled Probe

To identify extended cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (Tm) is calculated using the formula: $Tm=81.5+16.6(\log [Na+])+0.41(fraction\ G+C)-(600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $Tm=81.5+16.6(\log [Na+])+0.41(fraction\ G+C)-(0.63\%\ formamide)-(600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook et al., supra.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the Tm. For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the Tm. Preferably, for hybridizations in 6X SSC, the

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hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions.

Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

Extended cDNAs, nucleic acids homologous to extended cDNAs or 5' ESTs, or genomic DNAs which have hybridized to the probe are identified by autoradiography or other conventional techniques.

2. Obtention of Extended cDNA or Genomic cDNA Sequences Having Lower Degrees of Homology to the Labeled Probe

The above procedure may be modified to identify extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a sodium concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide.

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Extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs which have hybridized to the probe are identified by autoradiography.

3. Determination of the Degree of Homology Between the Obtained Extended cDNAs and the Labeled Probe

If it is desired to obtain nucleic acids homologous to extended cDNAs, such as allelic variants thereof or nucleic acids encoding proteins related to the proteins encoded by the extended cDNAs, the level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST used as the probe may be further determined using BLAST2N; parameters may be adapted depending on the sequence length and degree of homology studied. To determine the level of homology between the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived are compared. For example, using the above methods, nucleic acids having at least 95% nucleic acid homology to the extended cDNA or 5'EST from which the probe was derived may be obtained and identified. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA or 5'EST from which the probe was derived.

To determine whether a clone encodes a protein having a given amount of homology to the protein encoded by the extended cDNA or 5' EST, the amino acid sequence encoded by the extended cDNA or 5' EST is compared to the amino acid sequence encoded by the hybridizing nucleic acid. Homology is determined to exist when an amino acid sequence in the extended cDNA or 5' EST is closely related to an amino acid sequence in the hybridizing nucleic acid. A sequence is closely related when it is identical to that of the extended cDNA or 5' EST or when it contains one or more amino acid substitutions therein in which amino acids having similar characteristics have been substituted for one another. Using the above methods and algorithms such as FASTA with parameters depending on the sequence length and degree of homology studied, one can obtain nucleic acids encoding proteins having at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the proteins encoded by the extended cDNA or 5'EST from which the probe was derived.

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In addition to the above described methods, other protocols are available to obtain extended cDNAs using 5' ESTs as outlined in the following paragraphs.

Extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing polyA selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the polyA tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of SEQ ID NOs 38-270. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the sequences of SEQ ID NOs 38-270. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the sequences of SEQ ID NOs 38-270. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of SEQ ID NOs 38-270. If it is desired to obtain extended cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RT-PCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by hybridizing an mRNA comprising the sequence of the 5'EST for which an extended cDNA is desired with a primer comprising at least 10 consecutive nucleotides of the sequences complementary to the 5'EST and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the 5'EST. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the 5'EST.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or

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viral vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described *in Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997 and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989, the entire disclosures of which are incorporated herein by reference.

Alternatively, procedures such as the one described in Example 29 may be used for obtaining full length cDNAs or extended cDNAs. In this approach, full length or extended cDNAs are prepared from mRNA and cloned into double stranded phagemids as follows. The cDNA library in the double stranded phagemids is then rendered single stranded by treatment with an endonuclease, such as the Gene II product of the phage F1, and an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993). A biotinylated oligonucleotide comprising the sequence of a 5' EST, or a fragment containing at least 10 nucleotides thereof, is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the fragment comprises 20-30 consecutive nucleotides from the 5' EST. In some procedures, the fragment may comprise more than 30 consecutive nucleotides from the 5' EST.

Hybrids between the biotinylated oligonucleotide and phagemids having inserts containing the 5' EST sequence are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet (Fry *et al.*, *Biotechniques*, 13: 124-131, 1992). Therafter, the resulting phagemids containing the 5' EST sequence are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST sequence. Alternatively, protocoles such as the Gene Trapper kit (Gibco BRL) may be used. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs containing the 5' EST sequence are identified by colony PCR or colony hybridization.

Using any of the above described methods in section III, a plurality of extended cDNAs containing full length protein coding sequences or sequences encoding only the

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mature protein remaining after the signal peptide is cleaved off may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

IV. Expression of Proteins Encoded by Extended cDNAs Isolated Using 5′ ESTs

Extended cDNAs containing the full protein coding sequences of their corresponding mRNAs or portions thereof, such as cDNAs encoding the mature protein, may be used to express the encoded secreted proteins or portions thereof as described in Example 30 below. If desired, the extended cDNAs may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. It will be appreciated that a plurality of extended cDNAs containing the full protein coding sequences or portions thereof may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 30

Expression of the Proteins Encoded by the Genes Corresponding to 5'ESTS or Portions Thereof

To express the proteins encoded by the genes corresponding to 5′ ESTs (or portions thereof), full length cDNAs containing the entire protein coding region or extended cDNAs containing sequences adjacent to the 5′ ESTs (or portions thereof) are obtained as described in Examples 27-29 and cloned into a suitable expression vector. If desired, the nucleic acids may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and

codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, *et al.*, U.S. Patent No. 5,082,767, incorporated herein by this reference.

The cDNA cloned into the expression vector may encode the entire protein (*i.e.* the signal peptide and the mature protein), the mature protein (*i.e.* the protein created by cleaving the signal peptide off), only the signal peptide or any other portion thereof.

The following is provided as one exemplary method to express the proteins encoded by the extended cDNAs corresponding to the 5' ESTs or the nucleic acids described above. First, the methionine initiation codon for the gene and the polyA signal of the gene are identified. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the extended cDNA lacks a polyA signal, this sequence can be added to the construct by, for example, splicing out the polyA signal from pSG5 (Stratagene) using BglII and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The extended cDNA or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the extended cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5'primer and BglII at the 5' end of the corresponding cDNA 3' primer, taking care to ensure that the extended cDNA is positioned with the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1 containing a poly A signal and prepared for this ligation (blunt/BglII).

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 μg/ml G418 (Sigma, St. Louis, Missouri). Preferably the expressed protein is released into the culture medium, thereby facilitating purification.

Alternatively, the extended cDNAs may be cloned into pED6dpc2 as described above. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. Preferably, the protein expressed from the extended cDNA is released into the culture medium thereby facilitating purification.

Proteins in the culture medium are separated by gel electrophoresis. If desired, the proteins may be ammonium sulfate precipitated or separated based on size or charge prior to electrophoresis.

As a control, the expression vector lacking a cDNA insert is introduced into host cells or organisms and the proteins in the medium are harvested. The secreted proteins present in the medium are detected using techniques familiar to those skilled in the art such as Coomassie blue or silver staining or using antibodies against the protein encoded by the extended cDNA.

Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate 5' EST, extended cDNA, or portion thereof. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the 5' EST, extended cDNA, or portion thereof.

Secreted proteins from the host cells or organisms containing an expression vector which contains the extended cDNA derived from a 5' EST or a portion thereof are compared to those from the control cells or organism. The presence of a band in the medium from the cells containing the expression vector which is absent in the medium from the control cells indicates that the extended cDNA encodes a secreted protein. Generally, the band corresponding to the protein encoded by the extended cDNA will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, if the protein expressed from the above expression vectors does not contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector with an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in control host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression

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vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of
5   modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

The protein encoded by the extended cDNA may be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is
10   allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques.

If antibody production is not possible, the extended cDNA sequence or portion thereof may be incorporated into expression vectors designed for use in purification schemes
15   employing chimeric polypeptides. In such strategies, the coding sequence of the extended cDNA or portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β-globin or a nickel binding polypeptide. A chromatography matrix having antibody to β-globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β-globin
20   gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β-globin chimerics is pSG5 (Stratagene), which encodes rabbit β-globin. Intron II of the rabbit β-globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases
25   the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.., (Basic Methods in Molecular Biology*, Davis, Dibner, and Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using *in vitro*
30   translation systems such as the *In vitro* Express™ Translation Kit (Stratagene).

Following expression and purification of the secreted proteins encoded by the 5'
ESTs, extended cDNAs, or fragments thereof, the purified proteins may be tested for the
ability to bind to the surface of various cell types as described in Example 31 below. It will be
appreciated that a plurality of proteins expressed from these cDNAs may be included in a
5   panel of proteins to be simultaneously evaluated for the activities specifically described below,
as well as other biological roles for which assays for determining activity are available.

EXAMPLE 31

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

10   The proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof are
cloned into expression vectors such as those described in Example 30. The proteins are
purified by size, charge, immunochromatography or other techniques familiar to those skilled
in the art. Following purification, the proteins are labeled using techniques known to those
skilled in the art. The labeled proteins are incubated with cells or cell lines derived from a
15   variety of organs or tissues to allow the proteins to bind to any receptor present on the cell
surface. Following the incubation, the cells are washed to remove non-specifically bound
protein. The labeled proteins are detected by autoradiography. Alternatively, unlabeled
proteins may be incubated with the cells and detected with antibodies having a detectable
label, such as a fluorescent molecule, attached thereto.

20   Specificity of cell surface binding may be analyzed by conducting a competition
analysis in which various amounts of unlabeled protein are incubated along with the labeled
protein. The amount of labeled protein bound to the cell surface decreases as the amount of
competitive unlabeled protein increases. As a control, various amounts of an unlabeled
protein unrelated to the labeled protein is included in some binding reactions. The amount of
25   labeled protein bound to the cell surface does not decrease in binding reactions containing
increasing amounts of unrelated unlabeled protein, indicating that the protein encoded by the
cDNA binds specifically to the cell surface.

As discussed above, secreted proteins have been shown to have a number of
30   important physiological effects and, consequently, represent a valuable therapeutic resource.
The secreted proteins encoded by the extended cDNAs or portions thereof made according to

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Examples 27-29 may be evaluated to determine their physiological activities as described below.

EXAMPLE 32

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Cytokine,
Cell Proliferation or Cell Differentiation Activity

As discussed above, secreted proteins may act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein encoded by the extended cDNAs is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M⁻ (preB M⁻), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins encoded by the above extended cDNAs or portions thereof may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references, which are incorporated herein by reference: *Current Protocols in Immunology*, Ed. by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience; Takai *et al. J. Immunol.* 137:3494-3500, 1986., Bertagnolli *et al.*, J. *Immunol.* 145:1706-1712, 1990., Bertagnolli *et al.*, *Cell. Immunol.* 133:327-341, 1991; Bertagnolli, *et al.*, *J. Immunol.* 149:3778-3783, 1992; Bowman *et al.*, *J. Immunol.* 152:1756-1761, 1994.

In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology, supra* 1:3.12.1-3.12.14; and Schreiber In *Current Protocols in Immunology, supra* 1 : 6.8.1-6.8.8.

The proteins encoded by the cDNAs may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references, which are incorporated herein by reference: Bottomly *et al.*, In *Current Protocols in Immunology., supra.* 1 : 6.3.1-6.3.12,; deVries *et al.*, *J. Exp. Med.* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 36:690-692, 1988; Greenberger *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*

80:2931-2938, 1983; Nordan, R., In *Current Protocols in Immunology.*, *supra.* 1 : 6.6.1-6.6.5; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Bennett *et al.*, in *Current Protocols in Immunology supra* 1 : 6.15.1; Ciarletta *et al.*, In *Current Protocols in Immunology. supra* 1 : 6.13.1.

5   The proteins encoded by the cDNAs may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans)

10   in *Current Protocols in Immunology supra*; Weinberger *et al.*, *Proc. Natl. Acad. Sci. USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur. J. Immun.* 11:405-411, 1981; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988.

          Those proteins which exhibit cytokine, cell proliferation, or cell differentiation activity

15   may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

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EXAMPLE 33

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Activity as Immune System Regulators

          The proteins encoded by the cDNAs may also be evaluated for their effects as

25   immune regulators. For example, the proteins may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in *Current Protocols in*

30   *Immunology* , Coligan *et al.*, Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann *et al.*, *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann *et al.*, *J.*

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Immunol. **128**:1968-1974, 1982; Handa *et al., J. Immunol.* **135**:1564-1572, 1985; Takai *et al., J. Immunol.* **137**:3494-3500, 1986; Takai *et al., J. Immunol.* **140**:508-512, 1988; Bowman *et al., J. Virology* **61**:1992-1998; Bertagnolli *et al., Cell. Immunol.* **133**:327-341, 1991; Brown *et al., J. Immunol.* **153**:3079-3092, 1994.

5   The proteins encoded by the cDNAs may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Maliszewski, *J. Immunol.* **144**:3028-3033, 1990; Mond *et al.* in *Current Protocols in Immunology*, 1 : 3.8.1-3.8.16, *supra.*

10   The proteins encoded by the cDNAs may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) 15 in *Current Protocols in Immunology, supra*; Takai *et al., J. Immunol.* **137**:3494-3500, 1986; Takai *et al., J. Immunol.* **140**:508-512, 1988; Bertagnolli *et al., J. Immunol.* **149**:3778-3783, 1992.

The proteins encoded by the cDNAs may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are 20 familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Guery *et al., J. Immunol.* **134**:536-544, 1995; Inaba *et al., J. Exp. Med.* **173**:549-559, 1991; Macatonia *et al., J. Immunol.* **154**:5071-5079, 1995; Porgador *et al.J. Exp. Med* **182**:255-260, 1995; Nair *et al., J. Virol.* **67**:4062-4069, 1993; Huang *et al., Science* **264**:961-965, 1994; Macatonia *et al.J. Exp. Med* **169**:1255-25 1264, 1989; Bhardwaj *et al., Journal of Clinical Investigation* **94**:797-807, 1994; and Inaba *et al., J. Exp. Med* **172**:631-640, 1990.

The proteins encoded by the cDNAs may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein 30 by reference: Darzynkiewicz *et al., Cytometry* **13**:795-808, 1992; Gorczyca *et al., Leukemia* **7**:659-670, 1993; Gorczyca *et al., Cancer Res.* **53**:1945-1951, 1993; Itoh *et al., Cell* **66**:233-

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243, 1991; Zacharchuk, *J. Immunol.* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Int. J. Oncol.* 1:639-648, 1992.

The proteins encoded by the cDNAs may also be evaluated for their influence on early steps of T-cell commitment and development. Numerous assays for such activity are familiar to those skilled in the art, including without limitation the assays disclosed in the following references, which are incorporated herein by references: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell. Immunol.* 155:111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc. Nat. Acad Sci. USA* 88:7548-7551, 1991.

Those proteins which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., plamodium and various fungal infections such as candidiasis. Of course, in this regard, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Alternatively, proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may be used in treatment of autoimmune disorders including, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including,

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for example, organ transplantation), may also be treatable using a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses either up or down.

Down regulation may involve inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active non-antigen-specific process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after the end of exposure to the tolerizing agent. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions, such as, for example, B7 costimulation), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation, can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may

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avoid the·necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or
5　GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* 257:789-792, 1992 and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-
10　11105, 1992. In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that
15　are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor/ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of
20　autoantibodies or T cell-derived cytokines which potentially involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine
25　experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/pr/pr mice or NZB hybrid mice, murine autoimmuno collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *supra*, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of
30　immune responses may involve either enhancing an existing immune response or eliciting an initial immune response as shown by the following examples. For instance, enhancing an

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immune response through stimulating B lymphocyte antigen function may be useful in cases
of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and
encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte
antigens systemically.

5   Alternatively, antiviral immune responses may be enhanced in an infected patient by
removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed
APCs either expressing a peptide encoded by extended cDNAs derived from the 5' ESTs of
the present invention or together with a stimulatory form of a soluble peptide encoded by
extended cDNAs derived from the 5' ESTs of the present invention and reintroducing the *in*
10   *vitro* primed T cells into the patient. The infected cells would now be capable of delivering a
costimulatory signal to T cells *in vivo*, thereby activating the T cells.

In another application, upregulation or enhancement of antigen function (preferably B
lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells
(e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with
15   a nucleic acid encoding at least one peptide encoded by extended cDNAs derived from the 5'
ESTs of the present invention can be administered to a subject to overcome tumor-specific
tolerance in the subject. If desired, the tumor cell can be transfected to express a combination
of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with
an expression vector directing the expression of a peptide having B7-2-like activity alone, or
20   in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The
transfected tumor cells are returned to the patient to result in expression of the peptides on
the surface of the transfected cell. Alternatively, gene therapy techniques can be used to
target a tumor cell for transfection *in vivo*.

The presence of the peptide encoded by extended cDNAs derived from the 5' ESTs
25   of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the
tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated
immune response against the transfected tumor cells. In addition, tumor cells which lack or
which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules can be
transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain
30   truncated portion) of an MHC class I α chain and β_2 microglobulin or an MHC class II α
chain and an MHC class II β chain to thereby express MHC class I or MHC class II proteins

on the cell surface, respectively. Expression of the appropriate MHC class I or class II molecules in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, genes encoding these immune system regulator proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 34

Assaying the Proteins Expressed from Extended cDNAs

or Portions Thereof for Hematopoiesis Regulating Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Johansson *et al. Cell. Biol.* 15:141-151, 1995; Keller *et al., Mol. Cell. Biol.* 13:473-486, 1993; McClanahan *et al., Blood* 81:2903-2915, 1993.

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Freshney, Methylcellulose Colony Forming Assays, in *Culture of Hematopoietic Cells.*, Freshney, *et al.*. Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama *et al., Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; McNiece and Briddell, in *Culture of Hematopoietic Cells,* *supra*; Neben *et al., Exp. Hematol.* 22:353-359, 1994; Ploemacher and Cobblestone In

*Culture of Hematopoietic Cells, supra*1-21, Spooncer *et al*, in *Culture of Hematopoietic Cells, supra*163-179 and Sutherland in *Culture of Hematopoietic Cells, supra*. 139-162.

Those proteins which exhibit hematopoiesis regulatory activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoeisis is beneficial, such as in the treatment of myeloid or lymphoid cell deficiencies. Involvement in regulating hematopoiesis is indicated even by marginal biological activity in support of colony forming cells or of factor-dependent cell lines. For example, proteins supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, indicates utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells. Proteins supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) may be useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression. Proteins supporting the growth and proliferation of megakaryocytes and consequently of platelets allows prevention or treatment of various platelet disorders such as thrombocytopenia, and generally may be used in place of or complementary to platelet transfusions. Proteins supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells may therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantion, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in vivo* or *ex vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, genes encoding hematopoiesis regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 35

<u>Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof</u>

<u>for Regulation of Tissue Growth</u>

The proteins encoded by the extended cDNAs or portions thereof may also be
evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to
those skilled in the art, including the assays disclosed in International Patent Publication No.
WO95/16035, International Patent Publication No. WO95/05846 and International Patent
Publication No. WO91/07491, which are incorporated herein by reference.

Assays for wound healing activity include, without limitation, those described in:
Winter, *Epidermal Wound Healing*, pps. 71-112, Maibach and Rovee, eds., Year Book
Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, *J. Invest. Dermatol.*
71:382-84, 1978, which are incorporated herein by reference.

Those proteins which are involved in the regulation of tissue growth may then be
formulated as pharmaceuticals and used to treat clinical conditions in which regulation of
tissue growth is beneficial. For example, a protein encoded by extended cDNAs derived from
the 5' ESTs of the present invention also may have utility in compositions used for bone,
cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound
healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present
invention, which induces cartilage and/or bone growth in circumstances where bone is not
normally formed, has application in the healing of bone fractures and cartilage damage or
defects in humans and other animals. Such a preparation employing a protein of the invention
may have prophylactic use in closed as well as open fracture reduction and also in the
improved fixation of artificial joints. *De novo* bone synthesis induced by an osteogenic agent
contributes to the repair of congenital, trauma induced, or oncologic resection induced
craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease,
and in other tooth repair processes. Such agents may provide an environment to attract bone-
forming cells, stimulate growth of bone-forming cells or induce differentiation of bone-
forming cell progenitors. A protein of the invention may also be useful in the treatment of
osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or

by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein encoded by extended cDNAs derived from the 5' ESTs of the present invention is tendon/ligament formation. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition encoded by extended cDNAs derived from the 5' ESTs of the present invention contributes to the repair of tendon or ligaments defects of congenital, traumatic or other origin and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions encoded by extended cDNAs derived from the 5' ESTs of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.*, for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and

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Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein of the invention may also exhibit angiogenic activity.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, genes encoding tissue growth regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 36

Assaying the Proteins Expressed from Extended cDNAs or Portions
Thereof for Regulation of Reproductive Hormones

The proteins encoded by the extended cDNAs or portions thereof may also be
evaluated for their ability to regulate reproductive hormones, such as follicle stimulating
hormone. Numerous assays for such activity are familiar to those skilled in the art, including
the assays disclosed in the following references, which are incorporated herein by reference:
Vale et al., Endocrinol. 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et
al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al.,
Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986, Chapter 6.12 in Current Protocols in
Immunology, Coligan et al. Eds. Greene Publishing Associates and Wiley-Intersciece ; Taub
et al., J. Clin. Invest. 95:1370-1376, 1995; Lind et al., APMIS 103:140-146, 1995; Muller et
al., Eur. J. Immunol. 25:1744-1748; Gruber et al., J. Immunol. 152:5860-5867, 1994;
Johnston et al., J Immunol. 153:1762-1768, 1994.

Those proteins which exhibit activity as reproductive hormones or regulators of cell
movement may then be formulated as pharmaceuticals and used to treat clinical conditions in
which regulation of reproductive hormones are beneficial. For example, a protein encoded by
extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activin-
or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of
follicle stimulating hormone (FSH), while activins are characterized by their ability to
stimulate the release of FSH. Thus, a protein encoded by extended cDNAs derived from the
5' ESTs of the present invention, alone or in heterodimers with a member of the inhibin α
family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in
female mammals and decrease spermatogenesis in male mammals. Administration of
sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the
protein of the invention, as a homodimer or as a heterodimer with other protein subunits of
the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of
activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for
example, United States Patent 4,798,885, the disclosure of which is incorporated herein by
reference. A protein of the invention may also be useful for advancement of the onset of

fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, genes encoding reproductive hormone regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 37

Assaying the Proteins Expressed from Extended cDNAs or
Portions Thereof for Chemotactic/Chemokinetic Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for chemotactic/chemokinetic activity. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of

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cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by Coligan, Kruisbeek, Margulies, Shevach and Strober, Pub. Greene Publishing Associates and Wiley-Interscience, Chapter **6.12**: 6.12.1-6.12.28; Taub *et al., J. Clin. Invest.* 95:1370-1376, 1995; Lind *et al., APMIS* 103:140-146, 1995; Mueller *et al., Eur. J. Immunol.* 25:1744-1748; Gruber *et al., J. Immunol.* 152:5860-5867, 1994; Johnston *et al. J. Immunol.*, 153:1762-1768, 1994.

EXAMPLE 38

Assaying the Proteins Expressed from Extended cDNAs or

Portions Thereof for Regulation of Blood Clotting

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.* 45:413-419, 1987; Humphrey *et al., Fibrinolysis* 5:71-79, 1991; Schaub, *Prostaglandins* 35:467-474, 1988.

Those proteins which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as infarction of cardiac and central nervous system vessels (e.g., stroke)). Alternatively, as described in more detail below, genes encoding blood clotting activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

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EXAMPLE 39

Assaying the Proteins Expressed from Extended cDNAs or

Portions Thereof for Involvement in Receptor/Ligand Interactions

The proteins encoded by the extended cDNAs or a portion thereof may also be
evaluated for their involvement in receptor/ligand interactions. Numerous assays for such
involvement are familiar to those skilled in the art, including the assays disclosed in the
following references, which are incorporated herein by reference: Chapter 7. 7.28.1-7.28.22
in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and
Wiley-Interscience; Takai *et al.*, *Proc. Natl. Acad. Sci. USA* **84**:6864-6868, 1987; Bierer *et
al.*, *J. Exp. Med.* **168**:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* **169**:149-160, 1989;
Stoltenborg *et al.*, *J. Immunol. Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995;
Gyuris *et al.*, *Cell* 75:791-803, 1993.

For example, the proteins encoded by extended cDNAs derived from the 5' ESTs of
the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors
or agonists of receptor/ligand interactions. Examples of such receptors and ligands include,
without limitation, cytokine receptors and their ligands, receptor kinases and their ligands,
receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their
ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins
and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen
recognition and development of cellular and humoral immune responses). Receptors and
ligands are also useful for screening of potential peptide or small molecule inhibitors of the
relevant receptor/ligand interaction. A protein encoded by extended cDNAs derived from the
5' ESTs of the present invention (including, without limitation, fragments of receptors and
ligands) may themselves be useful as inhibitors of receptor/ligand interactions. Alternatively,
as described in more detail below, genes encoding proteins involved in receptor/ligand
interactions or nucleic acids regulating the expression of such proteins may be introduced into
appropriate host cells to increase or decrease the expression of the proteins as desired.

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EXAMPLE 40

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof

for Anti-Inflammatory Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be

evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by

providing a stimulus to cells involved in the inflammatory response, by inhibiting or

promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or

promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting

cell extravasation, or by stimulating or suppressing production of other factors which more

directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can

be used to treat inflammatory conditions including chronic or acute conditions, including

without limitation inflammation associated with infection (such as septic shock, sepsis or

systemic inflammatory response syndrome), ischemia-reperfusioninury, endotoxin lethality,

arthritis, complement-mediated hyperacute rejection, nephritis, cytokine- or chemokine-

induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over

production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to

treat anaphylaxis and hypersensitivity to an antigenic substance or material. Alternatively, as

described in more detail below, genes encoding anti-inflammatory activity proteins or nucleic

acids regulating the expression of such proteins may be introduced into appropriate host cells

to increase or decrease the expression of the proteins as desired.

EXAMPLE 41

Assaying the Proteins Expressed from Extended cDNAs or

Portions Thereof for Tumor Inhibition Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be

evaluated for tumor inhibition activity. In addition to the activities described above for

immunological treatment or prevention of tumors, a protein of the invention may exhibit other

anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for

example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor

tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor

growth (such as, for example, by inhibiting angiogenesis), by causing production of other

factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth. Alternatively, as described in more detail below, genes tumor inhibition activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to
5   increase or decrease the expression of the proteins as desired.

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting
10   (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism,
15   processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and
20   growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune
25   response against such protein or another material or entity which is cross-reactive with such protein. Alternatively, as described in more detail below, genes encoding proteins involved in any of the above mentioned activities or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.
30

EXAMPLE 42

Identification of Proteins which Interact with

Polypeptides Encoded by Extended cDNAs

Proteins which interact with the polypeptides encoded by cDNAs derived from the 5'
ESTs or fragments thereof, such as receptor proteins, may be identified using two hybrid
systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech).
As described in the manual accompanying the kit which is incorporated herein by reference,
the the cDNAs derived from 5' ESTs, or fragments thereof, are inserted into an expression
vector such that they are in frame with DNA encoding the DNA binding domain of the yeast
transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins which
might interact with the polypeptides encoded by the extended cDNAs or portions thereof are
inserted into a second expression vector such that they are in frame with DNA encoding the
activation domain of GAL4. The two expression plasmids are transformed into yeast and the
yeast are plated on selection medium which selects for expression of selectable markers on
each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene.
Transformants capable of growing on medium lacking histidine are screened for GAL4
dependent lacZ expression. Those cells which are positive in both the histidine selection and
the lacZ assay contain plasmids encoding proteins which interact with the polypeptide
encoded by the extended cDNAs or portions thereof.

Alternatively, the system described in Lustig *et al.*, *Methods in Enzymology* **283**: 83-
99, 1997, and in U.S. Patent No. 5,654,150, the disclosure of which is incorporated herein by
reference, may be used for identifying molecules which interact with the polypeptides
encoded by extended cDNAs. In such systems, *in vitro* transcription reactions are performed
on a pool of vectors containing extended cDNA inserts cloned downstream of a promoter
which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into
Xenopus laevis oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above
may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a
desired activity or for interaction with a known polypeptide.

Proteins or other molecules interacting with polypeptides encoded by extended
cDNAs can be found by a variety of additional techniques. In one method, affinity

columns containing the polypeptide encoded by the extended cDNA or a portion thereof can be constructed. In some versions, of this method the affinity column contains chimeric proteins in which the protein encoded by the extended cDNA or a portion thereof is fused to glutathione S-transferase. A mixture of cellular proteins or pool of

5   expressed proteins as described above and is applied to the affinity column. Proteins interacting with the polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen *et al.*, *Electrophoresis* **18**:588-598, 1997, the disclosure of which is incorporated herein by reference. Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods

10   and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Proteins interacting with polypeptides encoded by extended cDNAs or portions thereof can also be screened by using an Optical Biosensor as described in Edwards and Leatherbarrow, *Analytical Biochemistry* **246**:1-6, 1997, the disclosure of which is

15   incorporated herein by reference. The main advantage of the method is that it allows the determination of the association rate between the protein and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethl dextran matrix) and a sample of test molecules is placed in contact with

20   the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extend a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the polypeptides encoded by extended cDNAs or a portion thereof and the test

25   sample can be a collection of proteins extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test proteins are extracted can originate from any species.

In other methods, a target protein is immobilized and the test population is a

30   collection of unique polypeptides encoded by the extended cDNAs or portions thereof.

To study the interaction of the proteins encoded by the extended cDNAs or portions thereof with drugs, the microdialysis coupled to HPLC method described by Wang *et al.*, *Chromatographia* 44:205-208, 1997 or the affinity capillary electrophoresis method described by Busch *et al.*, *J. Chromatogr.* 777:311-328, 1997, the disclosures of which are incorporated herein by reference can be used.

It will be appreciated by those skilled in the art that the proteins expressed from the extended cDNAs or portions may be assayed for numerous activities in addition to those specifically enumerated above. For example, the expressed proteins may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins expressed from the extended cDNAs or portions thereof may be useful as nutritional agents or cosmetic agents.

The proteins expressed from the cDNAs or portions thereof may be used to generate antibodies capable of specifically binding to the expressed protein or fragments thereof as described in Example 40 below. The antibodies may capable of binding a full length protein encoded by a cDNA derived from a 5' EST, a mature protein (*i.e.* the protein generated by cleavage of the signal peptide) encoded by a cDNA derived from a 5' EST, or a signal peptide encoded by a cDNA derived from a 5' EST. Alternatively, the antibodies may be capable of binding fragments of at least 10 amino acids of the proteins encoded by the above cDNAs. In some embodiments, the antibodies may be capable of binding fragments of at least 15 amino acids of the proteins encoded by the above cDNAs. In other embodiments, the antibodies may be capable of binding fragments of at least 25 amino acids of the proteins expressed from the extended cDNAs which comprise at least 25 amino acids of the proteins encoded by the above cDNAs. In further embodiments, the antibodies may be capable of binding fragments of at least 40 amino acids of the proteins encoded by the above cDNAs.

EXAMPLE 43

Production of an Antibody to a Human Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells as described in Example 30. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the

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level of a few μg/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

1. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, and Milstein, *Nature* 256:495, 1975 or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419, 1980, the disclosure of which is incorporated herein by reference and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis *et al.* in *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2, the disclosure of which is incorporated herein by reference.

2. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals response vary depending on site of inoculations and doses, with both inadequate or

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excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis. *et al*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971) , the disclosure of which is incorporated herein by reference..

5   Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, *et al.*, Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973) , the disclosure of which is incorporated herein by reference. Plateau

10   concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980) , the disclosure of which is incorporated herein by reference..

15   Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of

20   the protein in the body.

V. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof as Reagents

           The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable

25   therefrom) may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, sequences from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be used to design PCR primers to be used in isolation,

30   diagnostic, or forensic procedures.

1. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Isolation,
Diagnostic and Forensic Procedures

EXAMPLE 44

Preparation of PCR Primers and Amplification of DNA

The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. The PCR primers are at least 10 bases, and preferably at least 12, 15, or 17 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering, White Ed. *in Methods in Molecular Biology* **67**: Humana Press, Totowa 1997, the disclosure of which is incorporated herein by reference. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 45

Use of 5'ESTs as Probes

Probes derived from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), including full length cDNAs or genomic sequences, may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including *in vitro* transcription, nick

translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose

5   or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic

10   acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 30 above.

15   PCR primers made as described in Example 44 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 46-50 below. Such analyses may utilize detectable probes or primers based on the sequences of the the 5' ESTs or of cDNAs or genomic DNAs isolated using the 5' ESTs.

20   **EXAMPLE 46**

                          Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the 5' ESTs of Example 25, or cDNAs or genomic DNAs isolated

25   therefrom as described above, is then utilized in accordance with Example 44 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample.

30   Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example,

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with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 47

Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of 5'EST sequences from Example 25, or cDNA or genomic DNA sequences obtainable therefrom. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 44. Each of these DNA segments is sequenced, using the methods set forth in Example 46. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 48

Southern Blot Forensic Identification

The procedure of Example 47 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis *et al.* (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65), the disclosure of which is incorporated herein by reference..

A panel of probes based on the sequences of 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), or fragments thereof of at least 10 bases, are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis *et al.*,

5   supra). Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom).

10   Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the

15   number of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 49

20   Dot Blot Identification Procedure

Another technique for identifying individuals using the 5' EST sequences disclosed herein utilizes a dot blot hybridization technique.

Genomic DNA is isolated from nuclei of subject to be identified. Oligonucleotide probes of approximately 30 bp in length are synthesized that correspond to at least 10,

25   preferably 50 sequences from the 5' ESTs or cDNAs or genomic DNAs obtainable therefrom. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P^{32} using polynucleotide kinase (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose

30   filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis et *al.*, *supra*). The ^{32}P

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labeled DNA fragments are sequentially hybridized with successively stringent conditions to detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood *et al.*, *Proc. Natl. Acad. Sci. USA* **82(6)**:1585-1588, 1985) which is hereby incorporated by reference. A unique pattern of dots distinguishes one individual from another individual.

5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) or oligonucleotides containing at least 10 consecutive bases from these sequences can be used as probes in the following alternative fingerprinting technique. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, a plurality of probes having sequences from different genes are used in the alternative fingerprinting technique. Example 50 below provides a representative alternative fingerprinting procedure in which the probes are derived from 5'EST.

EXAMPLE 50

Alternative "Fingerprint" Identification Technique

20-mer oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, of 5'EST using commercially available oligonucleotide services such as Genset, Paris, France. Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with ^{32}P. The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes.

Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

The proteins encoded by the extended cDNAs may also be used to generate antibodies as explained in Examples 30 and 43 in order to identify the tissue type or cell species from which a sample is derived as described in example 51.

EXAMPLE 51

Identification of Tissue Types or Cell Species by Means of
Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations according to Examples 30 and 43 which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

A. Immunohistochemical techniques

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, Chap. 26 in: *Basic and Clinical Immunology*, 3rd Ed. Lange, Los Altos, California, 1980, or Rose, *et al.*, Chap. 12 in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley and Sons, New York (1980), the disclosures of which are incorporated herein by reference.

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin

5   or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ^{125}I, and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal

10   antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about

15   4 μm, unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

20   Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or

25   enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that

30   signal using appropriate standards.

B. Identification of tissue specific soluble proteins

The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, *et al.*, Section 19-2 in: *Basic Methods in Molecular Biology*, Leder ed., Elsevier, New York, 1986, the disclosure of which is incorporated herein by reference, using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5 to 55 μl, and containing from about 1 to 100 μg protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. *et al.*, *supra* Section 19-3. One set of nitrocellulose blots is stained with Coomassie blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 30 and 43. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

In either procedure A or B, a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other

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approaches, either the primary or secondary antibody is conjugated to a biotin molecule, which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

5   The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, prepared from the gene sequences identified from extended cDNA sequences, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

10   In addition to their applications in forensics and identification, 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be mapped to their chromosomal locations. Example 52 below describes radiation hybrid (RH) mapping of human chromosomal regions using 5'ESTs. Example 53 below describes a representative procedure for mapping an 5' EST to its location on a human chromosome. Example 54 below describes mapping of 5'

15   ESTs on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH). Those skilled in the art will appreciate that the method of Examples 52-54 may also be used to map cDNAs or genomic DNAs obtainable from the 5' ESTs to their chromosomal locations.

2. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Chromosome Mapping

20   EXAMPLE 52

Radiation hybrid mapping of 5'ESTs to the human genome

Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into

25   fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human genome. This technique is described by Benham et al., Genomics 4:509-517, 1989; and Cox et al., Science 250:245-250, 1990, the entire contents of which are hereby incorporated by reference. The random and independent nature of the subclones permits efficient mapping of

any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering 5'EST. In this approach, the frequency of breakage between markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs (Schuler *et al.*, *Science* 274:540-546, 1996, hereby incorporated by reference).

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH) and thymidine kinase (TK) (Foster *et al.*, *Genomics* 33:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr *et al.*, *Eur. J. Hum. Genet.* 4:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers *et al.*, *Genomics* 29:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer *et al.*, *Genomics* 14:574-584, 1992) and 13 loci on the long arm of chromosome 5 (Warrington *et al.*, *Genomics* 11:701-708, 1991).

                                    EXAMPLE 53

          Mapping of 5'ESTs to HumanChromosomes using PCR techniques

5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be assigned to human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich in *PCR Technology, Principles and Applications for DNA Amplification*, Freeman and Co., New York, 1992, the disclosure of which is incorporated herein by reference..

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase, and 1 µCu of a ^{32}P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified

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products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance between the ends of the primer sequences in the extended cDNA from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-

5   rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets of human chromosomes for the presence of a given 5' EST (or cDNA or genomic DNA obtainable therefrom). DNA is isolated from the somatic hybrids and used as starting

10   templates for PCR reactions using the primer pairs from the 5' EST (or cDNA or genomic DNA obtainable therefrom). Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the 5' EST (or cDNA or genomic DNA obtainable therefrom) will yield an amplified fragment. The 5' EST (or cDNA or genomic DNA obtainable therefrom) are assigned to a chromosome by analysis of the segregation pattern of

15   PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that 5'EST (or cDNA or genomic DNA obtainable therefrom). For a review of techniques and analysis of results from somatic cell gene mapping experiments, see Ledbetter *et al.*, *Genomics* 6:475-481, 1990, the disclosure of which is incorporated herein by reference.

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EXAMPLE 54

Mapping of Extended 5' ESTs to Chromosomes Using Fluorescence *In Situ* Hybridization

Fluorescence in situ hybridization allows the 5'EST (or cDNA or genomic DNA

25   obtainable therefrom) to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of an 5'EST (or cDNA or genomic DNA obtainable therefrom) is obtained by FISH as described by Cherif *et al.* (*Proc.*

30   *Natl. Acad. Sci. U.S.A.*, 87:6639-6643, 1990) , the disclosure of which is incorporated herein by reference.. Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-

stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μM) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BrdU, 0.1 mM) for 6 h. Colcemid (1 μg/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The 5'EST (or cDNA or genomic DNA obtainable therefrom) is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia, Upsala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μg/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 μg/100 ml in 20 mM Tris-HCl, 2 mM CaCl₂) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif *et al.*, *supra*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) may be localized to a particular cytogenetic R-band on a given chromosome.

Once the 5'EST (or cDNA or genomic DNA obtainable therefrom) have been assigned to particular chromosomes using the techniques described in Examples 52-54 above,

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they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 55

5   Use of 5'EST to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial

10   chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which the extended cDNAs (or genomic DNAs obtainable therefrom) are obtained. This approach is described in Nagaraja *et al., Genome Research* 7:210-222, 1997, the disclosure of which is incorporated herein by reference. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector.

15   The YAC inserts are screened using PCR or other methods to determine whether they include the 5'EST (or cDNA or genomic DNA obtainable therefrom) whose position is to be determined. Once an insert has been found which includes the 5'EST (or cDNA or genomic DNA obtainable therefrom), the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome

20   or in the region from which the 5'EST (or cDNA or genomic DNA obtainable therefrom) was derived. This process can be repeated for each insert in the YAC library to determine the location of each of the extended cDNAs (or genomic DNAs obtainable therefrom) relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may

25   be obtained.

As described in Example 56 below extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

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3. Use of 5'ESTs or Sequences Obtained Therefrom or Fragments Thereof in Gene Identification

EXAMPLE 56

Identification of genes associated with hereditary diseases or drug response

5   This example illustrates an approach useful for the association of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) with particular phenotypic characteristics. In this example, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) is used as a test probe to associate that 5'EST (or cDNA or genomic DNA obtainable therefrom) with a particular phenotypic characteristic.

10   5'ESTs (or cDNA or genomic DNA obtainable therefrom) are mapped to a particular location on a human chromosome using techniques such as those described in Examples 52 and 53 or other techniques known in the art. A search of Mendelian Inheritance in Man (McKusick in *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which

15   contains the 5'EST (or cDNA or genomic DNA obtainable therefrom) to be a very gene rich region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this 5'EST (or cDNA or genomic DNA obtainable therefrom) thus becomes an immediate candidate for each of these genetic diseases.

20   Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the 5'EST (or cDNA or genomic DNA obtainable therefrom) are used to screen genomic DNA, mRNA or cDNA obtained from the patients. 5'ESTs (or cDNA or genomic DNA obtainable therefrom) that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR

25   analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the 5'EST may be responsible for the genetic disease.

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VI. Use of 5'EST (or cDNA or Genomic DNA Obtainable Therefrom) to Construct Vectors

The present 5'ESTs (or cDNA or genomic DNA obtainable therefrom) may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes therein. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 57 below.

1. Construction of Secretion Vectors

EXAMPLE 57

Construction of Secretion Vectors

The secretion vectors include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from a 5' EST (or cDNAs or genomic DNAs obtainable therefrom) is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the 5' EST (or cDNA or genomic DNA obtainable therefrom). Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Many nucleic acid backbones suitable for

use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

The 5' ESTs may also be used to clone sequences located upstream of the 5' ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 58 describes a method for cloning sequences upstream of the extended cDNAs or 5' ESTs.

2. Identification of Upstream Sequences With Promoting or Regulatory Activities

EXAMPLE 58

Use of Extended cDNAs or 5' ESTs to Clone Upstream Sequences from Genomic DNA

Sequences derived from extended cDNAs or 5' ESTs may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions (which are incorporated herein by reference) using an outer adaptor primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for the extended cDNA or 5' EST of interest and should have a melting temperature, length, and location in the extended cDNA or 5'EST which is consistent with its use in PCR reactions. Each first PCR reaction contains 5 ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adaptor primer and outer gene specific primer, 1.1 mM of Mg(OAc)$_2$, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (7 cycles) / 2 sec - 94°C, 3 min - 67°C (32 cycles) / 5 min - 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested primer is specific for the adaptor, and is provided with the GenomeWalker™ kit. The second nested primer is specific for the particular extended cDNA or 5' EST for which the promoter is to be cloned and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR

reactions. The reaction parameters of the second PCR reaction are as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (6 cycles) / 2 sec - 94°C, 3 min - 67°C (25 cycles) / 5 min - 67°C. The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques.

Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated oligonucleotide comprising at least 15 nucleotides from the extended cDNA or 5' EST sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the extended cDNA or EST sequence are isolated as described in Example 29 above. Thereafter, the single stranded DNA containing the extended cDNA or EST sequence is released from the beads and converted into double stranded DNA using a primer specific for the extended cDNA or 5' EST sequence or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. DNAs containing the 5' EST or extended cDNA sequences are identified by colony PCR or colony hybridization.

Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the extended cDNAs or 5' ESTs with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example .

EXAMPLE 59

Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the extended cDNAs or 5' ESTs are cloned into a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, pβgal-Basic, pβgal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech. Briefly, each of these promoter reporter vectors include multiple cloning sites positioned

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upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, β galactosidase, or green fluorescent protein. The sequences upstream of the extended cDNAs or 5' ESTs are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained from a vector which lacks an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert. If necessary, the upstream sequences can be cloned into vectors which contain an enhancer for augmenting transcription levels from weak promoter sequences. A significant level of expression above that observed with the vector lacking an insert indicates that a promoter sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the results of the above described determination of expression patterns of the extended cDNAs and ESTs. For example, if the expression pattern analysis indicates that the mRNA corresponding to a particular extended cDNA or 5' EST is expressed in fibroblasts, the promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by constructing nested deletions in the upstream DNA using conventional techniques such as Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether the deletion has reduced or obliterated promoter activity. In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 60

Cloning and Identification of Promoters

Using the method described in Example 58 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA

TTG CCT G (SEQ ID NO:29) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:30), the promoter having the internal designation P13H2 (SEQ ID NO:31) was obtained.

Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:32) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:33), the promoter having the internal designation P15B4 (SEQ ID NO:34) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:35) and GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:36), the promoter having the internal designation P29B6 (SEQ ID NO:37) was obtained.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start sites using the computer program MatInspector release 2.0, August 1996.

Table VII describes the transcription factor binding sites present in each of these promoters. The columns labeled matrice provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site found.

Bacterial clones containing plasmids containing the promoter sequences described above described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography.

The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The promoters and other regulatory sequences located upstream of the extended cDNAs or 5' ESTs may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described in Example 26 above. For example, if a promoter which confers a high level of expression in muscle is desired, the promoter sequence upstream of an extended cDNA or 5' EST derived from an mRNA which is expressed at a high level in muscle, as determined by the method of Example 26, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences using the procedures of Examples 58-60, proteins which interact with the promoter may be identified as described in Example 61 below.

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EXAMPLE 61

Identification of Proteins Which Interact with Promoter Sequences, Upstream
Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art.

Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1), the disclosure of which is incorporated herein by reference. Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem. A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression vectors or *in vitro* transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNAse protection analysis.

VII. Use of 5' ESTs (or cDNAs or Genomic DNAs Obtainable Therefrom) in Gene Therapy

The present invention also comprises the use of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) in gene therapy strategies, including antisense and triple helix strategies

5   as described in Examples 62 and 63 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences

10   may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

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EXAMPLE 62

Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the

20   5'EST (or cDNA or genomic DNA obtainable therefrom). The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular duplex with sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green *et al.*, *Ann. Rev. Biochem.* 55:569-597, 1986; and Izant and Weintraub, *Cell* 36:1007-1015,

25   1984, which are hereby incorporated by reference.

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using *in vitro* transcription systems such as

30   those which employ T7 or SP6 polymerase to generate the transcript. Another approach

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involves transcription of the antisense nucleic acids *in vivo* by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized *in vitro*. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity. Examples of modifications suitable for use in antisense strategies are described by Rossi *et al.*, *Pharmacol. Ther.* 50(2):245-254, 1991, which is hereby incorporated by reference.

Various types of antisense oligonucleotides complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom) may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026, hereby incorporated by reference, are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141, hereby incorporated by reference, are used.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523, hereby incorporated by reference, are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages, wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522, incorporated by reference, may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefore. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2, hereby incorporated by reference are used. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732, hereby incorporated by reference, is also contemplated. Because these molecules have no free ends, they are more resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using *in vitro* expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection, transfection or h-region-mediated import using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsidated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors, vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between 1×10^{-10}M to 1×10^{-4}M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide

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approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi *et al.*, *supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, a portion of 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences from the 5'EST or from the gene corresponding to the 5'EST are contemplated within the scope of this invention.

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EXAMPLE 63

Preparation and Use of Triple Helix Probes

The sequences of the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target gene corresponding to the extended cDNA from which the oligonucleotide was derived with known gene sequences that have been associated with a particular function. The cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the extended cDNA is associated with the disease using techniques described in Example 56.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced *in vivo* using the techniques described above and in Example 62 at a dosage calculated based on the *in vitro* results, as described in Example 62.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the

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generation of oligonucleotides suitable for triple helix formation see Griffin *et al.*, *Science* 245:967-971, 1989, which is hereby incorporated by this reference.

EXAMPLE 64

Use of cDNAs Obtained Using the 5' ESTs to Express an Encoded Protein in a Host Organism

The cDNAs obtained as described above using the 5' ESTs of the present invention may also be used to express an encoded protein in a host organism to produce a beneficial effect. In such procedures, the encoded protein may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein may have any of the activities described above. The encoded protein may be a protein which the host organism lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

A full length extended cDNA encoding the signal peptide and the mature protein, or an extended cDNA encoding only the mature protein is introduced into the host organism. The extended cDNA may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the extended cDNA may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors. The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein to produce a beneficial effect.

EXAMPLE 65

Use of Signal Peptides Encoded by 5' ESTs or Sequences obtained Therefrom
to Import Proteins Into Cells

The short core hydrophobic region (h) of signal peptides encoded by the 5'ESTS or
extended cDNAs derived from SEQ ID NOs: 38-270 may also be used as a carrier to import
a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al.*, *J. Biol.
Chem.*, **270**: 14225-14258, 1995; Du *et al.*, *J. Peptide Res.*, **51**: 235-243, 1998; Rojas *et al.*,
Nature Biotech., **16**: 370-375, 1998).

When cell permeable peptides of limited size (approximately up to 25 amino acids)
are to be translocated across cell membrane, chemical synthesis may be used in order to add
the h region to either the C-terminus or the N-terminus to the cargo peptide of interest.
Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can
be genetically engineered, using techniques familiar to those skilled in the art, in order to link
the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA
sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then
translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional
techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then
simply incubated with the cell permeable polypeptide which is then translocated across the
membrane.

This method may be applied to study diverse intracellular functions and cellular
processes. For instance, it has been used to probe functionally relevant domains of
intracellular proteins and to examine protein-protein interactions involved in signal
transduction pathways (Lin *et al.*, *supra*; Lin *et al.*, *J. Biol. Chem.*, **271**: 5305-5308, 1996;
Rojas *et al.*, *J. Biol. Chem.*, **271**: 27456-27461, 1996; Liu *et al.*, *Proc. Natl. Acad. Sci. USA*,
93: 11819-11824, 1996; Rojas *et al.*, *Bioch. Biophys. Res. Commun.*, **234**: 675-680, 1997).

Such techniques may be used in cellular therapy to import proteins producing
therapeutic effects. For instance, cells isolated from a patient may be treated with imported
therapeutic proteins and then re-introduced into the host organism.

Alternatively, the h region of signal peptides of the present invention could be used in
combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such
oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form

triple helixes, as described in examples 62 and 63 respectively, in order to inhibit processing and/or maturation of a target cellular RNA.

As discussed above, the cDNAs or portions thereof obtained using the 5' ESTs of the present invention can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803, 1993, the disclosure of which is hereby incorporated by reference) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins

involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

5   Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation *Molecular Cloning; A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Sambrook,. Fritsch and Maniatis eds., 1989, and *Methods in Enzymology; Guide to Molecular Cloning Techniques*, Academic Press, Berger and Kimmel eds., 1987.

10   Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid

15   preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the

20   disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims. All documents cited herein are incorporated herein by reference in their entirety.

Step	Search characteristic		Selection Characteristics		
	Program	Strand	Parameters	Identity (%)	Length (bp)
miscellanaeous	blastn	both	S=61 X=16	90	17
tRNA	fasta	both	-	80	60
rRNA	blastn	both	S=108	80	40
mtRNA	blastn	both	S=108	80	40
Procaryotic	blastn	both	S=144	90	40
Fungal	blastn	both	S=144	90	40
Alu	fasta*	both	-	70	40
L1	blastn	both	S=72	70	40
Repeats	blastn	both	S=72	70	40
Promoters	blastn	top	S=54 X=16	90	15†
Vertebrate	fasta*	both	S=108	90	30
ESTs	blastn	both	S=108 X=16	90	30
Proteins	blastx¤	top	E=0.001	-	-

Table 1: Parameters used for each step of EST analysis

* use "Quick Fast" Database scanner

† alignement further constrained to begin closer than 10bp to EST'5' end

¤ using BLOSUM62 substitution matrix

TABLE II

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID38	new	10.8	Brain	33-19-2-H2-PU
ID39	new	10.8	Brain	33-56-1-E8-PU
ID40	new	10	Brain	33-79-3-D12-PU
ID41	new	9.6	Brain	33-72-2-B2-PU
ID42	new	9.5	Brain	33-13-2-B9-PU
ID43	new	9.1	Brain	33-113-1-E9-PU
ID44	new	9	Brain	33-28-4-E8-PU
ID45	new	8.8	Brain	33-12-3-F2-PU
ID46	new	8.8	Brain	33-70-1-C11-PU
ID47	new	8.5	Brain	33-74-1-B2-PU
ID48	new	8.5	Brain	33-29-3-F1-PU
ID49	new	8.4	Brain	33-8-2-A1-PU
ID50	new	8.3	Brain	17-17-3-A9-PU
ID51	new	8.3	Brain	33-106-2-A8-PU
ID52	new	8.3	Brain	33-112-4-E7-PU
ID53	new	8.2	Brain	33-98-1-E6-PU
ID54	new	8.2	Brain	33-76-1-B6-PU
ID55	new	8	Brain	33-35-4-G8-PU
ID56	new	7.9	Brain	33-17-3-E4-PU
ID57	new	7.9	Brain	33-110-4-B5-PU
ID58	new	7.8	Brain	33-40-1-A11-PU
ID59	new	7.7	Brain	33-71-1-A8-PU
ID60	new	7.7	Brain	33-96-3-G7-PU
ID61	new	7.6	Brain	33-112-3-D12-PU
ID62	new	7.6	Brain	33-62-2-B3-PU
ID63	new	7.6	Brain	33-6-4-G6-PU
ID64	new	7.5	Brain	33-82-4-E2-PU
ID65	new	7.4	Brain	33-81-3-H11-PU
ID66	new	7.3	Brain	33-64-1-B4-PU
ID67	new	7.2	Brain	33-31-1-B12-PU
ID68	new	7	Brain	33-24-4-F9-PU
ID69	new	7	Brain	33-110-3-E9-PU
ID70	new	7	Brain	33-4-2-G5-PU
ID71	new	6.9	Brain	33-74-2-A4-PU
ID72	new	6.9	Brain	33-52-4-F9-PU
ID73	new	6.9	Brain	33-74-1-B11-PU
ID74	new	6.8	Brain	33-10-4-D9-PU
ID75	new	6.8	Brain	33-15-2-H3-PU
ID76	new	6.7	Brain	33-38-2-D5-PU
ID77	new	6.7	Brain	33-78-3-D2-PU
ID78	new	6.7	Brain	33-96-3-D3-PU
ID79	new	6.6	Brain	33-76-4-B11-PU
ID80	new	6.3	Brain	33-39-1-C6-PU
ID81	new	6.1	Brain	33-106-3-B12-PU
ID82	new	6	Brain	33-4-2-B7-PU
ID83	new	5.9	Brain	33-99-2-E4-PU
ID84	new	5.9	Brain	33-34-1-B1-PU
ID85	new	5.8	Brain	33-67-4-E9-PU
ID86	new	5.7	Brain	33-11-3-H11-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID87	new	5.6	Brain	33-13-2-A8-PU
ID88	new	5.6	Brain	33-83-4-B6-PU
ID89	new	5.6	Brain	33-70-1-E4-PU
ID90	new	5.6	Brain	33-5-3-H11-PU
ID91	new	5.6	Brain	33-10-3-G5-PU
ID92	new	5.5	Brain	33-97-4-G4-PU
ID93	new	5.5	Brain	33-46-4-F4-PU
ID94	new	5.4	Brain	33-4-1-G11-PU
ID95	new	5.3	Brain	33-105-1-H5-PU
ID96	new	5.3	Brain	33-74-2-B10-PU
ID97	new	5.3	Brain	33-49-3-E5-PU
ID98	new	5.3	Brain	33-114-2-A1-PU
ID99	new	5.2	Brain	33-71-1-G12-PU
ID100	new	5.2	Brain	33-47-3-E6-PU
ID101	new	5.2	Brain	33-1-2-E8-PU
ID102	new	5.2	Brain	33-93-4-E12-PU
ID103	new	5.1	Brain	33-1-2-H1-PU
ID104	new	5.1	Brain	17-10-1-H8-PU
ID105	new	5	Brain	33-110-2-B8-PU
ID106	new	5	Brain	33-104-3-D9-PU
ID107	new	5	Brain	33-72-2-H11-PU
ID108	new	4.9	Brain	33-7-4-D6-PU
ID109	new	4.9	Brain	33-31-4-G2-PU
ID110	new	4.9	Brain	33-109-1-E8-PU
ID111	new	4.8	Brain	17-1-2-B11-PU
ID112	new	4.8	Brain	33-19-4-H3-PU
ID113	new	4.8	Brain	33-14-4-E1-PU
ID114	new	4.8	Brain	33-70-3-H1-PU
ID115	new	4.7	Brain	33-86-4-H10-PU
ID116	new	4.7	Brain	33-107-3-D5-PU
ID117	new	4.7	Brain	33-23-4-B9-PU
ID118	new	4.7	Brain	33-82-4-H5-PU
ID119	new	4.6	Brain	33-16-3-F4-PU
ID120	new	4.6	Brain	33-97-4-C5-PU
ID121	new	4.6	Brain	33-100-3-B10-PU
ID122	new	4.6	Brain	33-59-3-E3-PU
ID123	new	4.5	Brain	33-25-1-G2-PU
ID124	new	4.5	Brain	17-16-3-B2-PU
ID125	new	4.4	Brain	33-52-4-E7-PU
ID126	new	4.4	Brain	33-91-1-D1-PU
ID127	new	4.4	Brain	33-26-1-B9-PU
ID128	new	4.4	Brain	33-97-3-H6-PU
ID129	new	4.4	Brain	33-109-2-E8-PU
ID130	new	4.3	Brain	33-59-2-B7-PU
ID131	new	4.3	Brain	33-28-4-D1-PU
ID132	new	4.3	Brain	33-29-4-E2-PU
ID133	new	4.1	Brain	33-70-1-H6-PU
ID134	new	4.1	Brain	33-7-1-B2-PU
ID135	new	4.1	Brain	33-52-4-F8-PU
ID136	new	4.1	Brain	33-23-2-A6-PU
ID137	new	4.1	Brain	33-39-3-E5-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID138	new	4.1	Brain	33-81-4-H6-PU
ID139	new	4.1	Brain	33-105-3-F5-PU
ID140	new	4	Brain	33-35-2-H11-PU
ID141	new	4	Brain	33-50-3-E12-PU
ID142	new	4	Brain	33-16-3-H7-PU
ID143	new	4	Brain	33-79-2-H4-PU
ID144	new	3.9	Brain	33-32-4-B12-PU
ID145	new	3.9	Brain	33-110-4-A5-PU
ID146	new	3.9	Brain	33-109-2-H1-PU
ID147	new	3.9	Brain	33-100-1-E6-PU
ID148	new	3.9	Brain	33-78-2-E7-PU
ID149	new	3.9	Brain	33-82-4-G3-PU
ID150	new	3.9	Brain	17-1-1-A9-PU
ID151	new	3.9	Brain	33-89-4-E1-PU
ID152	new	3.9	Brain	33-89-1-B4-PU
ID153	new	3.9	Brain	33-96-3-A3-PU
ID154	new	3.8	Brain	33-92-3-D1-PU
ID155	new	3.8	Brain	33-104-4-H4-PU
ID156	new	3.8	Brain	33-106-1-B8-PU
ID157	new	3.6	Brain	33-1-3-D1-PU
ID158	new	3.6	Brain	33-40-2-F5-PU
ID159	new	3.6	Brain	33-4-1-E8-PU
ID160	new	3.6	Brain	33-36-3-E2-PU
ID161	new	3.6	Brain	17-18-3-A6-PU
ID162	new	3.6	Brain	33-12-1-B1-PU
ID163	new	3.6	Brain	33-29-1-H1-PU
ID164	new	3.6	Brain	33-103-1-E1-PU
ID165	new	3.5	Brain	33-10-4-H2-PU
ID166	new	3.5	Brain	33-25-1-H2-PU
ID167	new	3.5	Brain	33-10-4-G2-PU
ID168	new	3.5	Brain	33-67-1-F4-PU
ID169	ext-est-not-vrt	12.5	Brain	33-77-4-E2-PU
ID170	ext-est-not-vrt	10.1	Brain	33-31-3-C11-PU
ID171	ext-est-not-vrt	9.8	Brain	33-28-2-H7-PU
ID172	ext-est-not-vrt	9.2	Brain	33-112-3-C8-PU
ID173	ext-est-not-vrt	7.9	Brain	33-23-3-A11-PU
ID174	ext-est-not-vrt	7.9	Brain	33-29-2-E11-PU
ID175	ext-est-not-vrt	7.9	Brain	33-66-4-C7-PU
ID176	ext-est-not-vrt	7.1	Brain	33-78-1-D7-PU
ID177	ext-est-not-vrt	6.6	Brain	33-31-3-D7-PU
ID178	ext-est-not-vrt	6.3	Brain	33-19-1-C11-PU
ID179	ext-est-not-vrt	6	Brain	33-67-1-A5-PU
ID180	ext-est-not-vrt	5.9	Brain	33-58-3-C8-PU
ID181	ext-est-not-vrt	4.9	Brain	33-107-4-C3-PU
ID182	ext-est-not-vrt	4.9	Brain	33-7-2-G12-PU
ID183	ext-est-not-vrt	4.8	Brain	33-11-1-G5-PU
ID184	ext-est-not-vrt	4.7	Brain	33-31-4-D9-PU
ID185	ext-est-not-vrt	4.6	Brain	33-26-4-E10-PU
ID186	ext-est-not-vrt	4.5	Brain	33-70-4-F7-PU
ID187	ext-est-not-vrt	4.5	Brain	33-19-2-D1-PU
ID188	ext-est-not-vrt	4.4	Brain	33-48-4-F8-PU

SEQ. ID NO.	CATEGORY	VON HELJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID189	ext-est-not-vrt	4.3	Brain	33-109-3-B10-PU
ID190	ext-est-not-vrt	4.1	Brain	33-30-2-A6-PU
ID191	ext-est-not-vrt	3.8	Brain	33-75-3-D7-PU
ID192	ext-est-not-vrt	3.7	Brain	33-109-4-C1-PU
ID193	est-not-ext	10.5	Brain	33-97-3-D4-PU
ID194	est-not-ext	10.1	Brain	33-61-2-F6-PU
ID195	est-not-ext	9.5	Brain	33-54-1-B9-PU
ID196	est-not-ext	9.3	Brain	33-39-4-D1-PU
ID197	est-not-ext	9.1	Brain	33-57-4-H5-PU
ID198	est-not-ext	9	Brain	33-60-2-B3-PU
ID199	est-not-ext	8.6	Brain	33-52-1-A1-PU
ID200	est-not-ext	8.4	Brain	33-82-2-H10-PU
ID201	est-not-ext	7.5	Brain	33-79-4-B11-PU
ID202	est-not-ext	7.5	Brain	33-18-3-H3-PU
ID203	est-not-ext	7.5	Brain	33-21-1-D6-PU
ID204	est-not-ext	7.4	Brain	33-17-3-F9-PU
ID205	est-not-ext	7.4	Brain	33-70-2-G3-PU
ID206	est-not-ext	7.4	Brain	33-89-3-H4-PU
ID207	est-not-ext	7.4	Brain	33-46-3-E10-PU
ID208	est-not-ext	7	Brain	33-36-2-F9-PU
ID209	est-not-ext	6.8	Brain	33-39-1-C4-PU
ID210	est-not-ext	6.8	Brain	33-65-4-C6-PU
ID211	est-not-ext	6.4	Brain	33-18-2-G6-PU
ID212	est-not-ext	6.4	Brain	33-36-3-C6-PU
ID213	est-not-ext	6	Brain	33-79-2-B6-PU
ID214	est-not-ext	5.9	Brain	33-71-4-D11-PU
ID215	est-not-ext	5.9	Brain	17-12-2-A3-PU
ID216	est-not-ext	5.9	Brain	33-95-1-A12-PU
ID217	est-not-ext	5.8	Brain	33-5-3-E3-PU
ID218	est-not-ext	5.8	Brain	33-74-2-D3-PU
ID219	est-not-ext	5.7	Brain	33-50-3-H8-PU
ID220	est-not-ext	5.6	Brain	33-19-1-A2-PU
ID221	est-not-ext	5.5	Brain	33-22-1-D3-PU
ID222	est-not-ext	5.5	Brain	33-97-1-G4-PU
ID223	est-not-ext	5.4	Brain	33-65-4-D10-PU
ID224	est-not-ext	5.4	Brain	33-79-4-C4-PU
ID225	est-not-ext	5.3	Brain	33-20-2-C5-PU
ID226	est-not-ext	5.2	Brain	33-34-4-A5-PU
ID227	est-not-ext	5.2	Brain	33-6-2-F11-PU
ID228	est-not-ext	5.2	Brain	33-2-2-G5-PU
ID229	est-not-ext	5.1	Brain	33-98-1-G7-PU
ID230	est-not-ext	5.1	Brain	33-20-3-B10-PU
ID231	est-not-ext	5	Brain	33-106-2-D9-PU
ID232	est-not-ext	4.9	Brain	33-72-2-A9-PU
ID233	est-not-ext	4.9	Brain	33-83-3-G8-PU
ID234	est-not-ext	4.8	Brain	33-31-3-E6-PU
ID235	est-not-ext	4.7	Brain	33-28-4-E2-PU
ID236	est-not-ext	4.6	Brain	33-101-3-F4-PU
ID237	est-not-ext	4.6	Brain	33-98-4-C1-PU
ID238	est-not-ext	4.5	Brain	33-31-2-E11-PU
ID239	est-not-ext	4.5	Brain	33-26-2-B6-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID240	est-not-ext	4.4	Brain	33-75-4-H7-PU
ID241	est-not-ext	4.3	Brain	33-13-1-C6-PU
ID242	est-not-ext	4.3	Brain	33-35-4-G1-PU
ID243	est-not-ext	4.3	Brain	33-76-3-G11-PU
ID244	est-not-ext	4.2	Brain	33-72-1-A3-PU
ID245	est-not-ext	4.2	Brain	33-71-2-A2-PU
ID246	est-not-ext	4.2	Brain	33-23-3-H10-PU
ID247	est-not-ext	4.2	Brain	33-13-1-C1-PU
ID248	est-not-ext	4.2	Brain	33-43-2-G12-PU
ID249	est-not-ext	4.2	Brain	33-91-4-E10-PU
ID250	est-not-ext	4.1	Brain	33-113-2-B8-PU
ID251	est-not-ext	4	Brain	33-104-3-G9-PU
ID252	est-not-ext	3.9	Brain	33-66-2-B10-PU
ID253	est-not-ext	3.9	Brain	33-1-2-E9-PU
ID254	est-not-ext	3.9	Brain	33-51-1-G7-PU
ID255	est-not-ext	3.9	Brain	33-32-3-D11-PU
ID256	est-not-ext	3.8	Brain	33-43-2-H10-PU
ID257	est-not-ext	3.8	Brain	33-48-4-H11-PU
ID258	est-not-ext	3.8	Brain	33-8-4-C5-PU
ID259	est-not-ext	3.8	Brain	33-24-1-F5-PU
ID260	est-not-ext	3.8	Brain	33-70-1-A9-PU
ID261	est-not-ext	3.8	Brain	33-30-4-C4-PU
ID262	est-not-ext	3.8	Brain	33-10-2-G7-PU
ID263	est-not-ext	3.6	Brain	33-18-4-E12-PU
ID264	est-not-ext	3.6	Brain	33-52-1-G7-PU
ID265	est-not-ext	3.6	Brain	33-57-1-H10-PU
ID266	est-not-ext	3.5	Brain	33-80-3-E2-PU
ID267	est-not-ext	3.5	Brain	33-36-1-D3-PU
ID268	ext-vrt-not-genomic	11.3	Brain	33-101-1-A2-PU
ID269	ext-vrt-not-genomic	6.6	Brain	33-55-2-E8-PU
ID270	ext-vrt-not-genomic	4.8	Brain	33-14-2-H3-PU

TABLE III

SEQ. ID
NO.   SIGNAL PEPTIDE

ID38   MLLLLGLCLGLSLC
ID39   MENGGAGTLQIRQVLLFFVLLGMSQA
ID40   MRGPEPGPQPTMEGDVLDTLEALGYKGPLLEEQALTKAAEGGLSSPEFSELCIWLGSQIK
              SLCNLEESITSAGRDDLESFQLEISGFLKEMACPYSVLISGDIKDRLKKKEDCLKLLLFL
              STELQA
ID41   MEKSWMLWNFVERWLIALASWSWALC
ID42   MQQTRTEAVAGAFSHCLGFCGMRLGLLLLARHWCIA
ID43   MEKGNAFLKNRLVVFLLLPLASGP
ID44   MFPFNQAGLPTLLMLIVFHAASMA
ID45   MTSRSLRRCSCLRVTHNKEILASTVSLGVEGYMLGGGSRINSSNLNDGEEECSPDSLLVW
              KKKSLLLWMSSLPSLG
ID46   MWTASAMDFRTCIASXLPALCYVQACRALMIAASVLGLPAILLLLTVLPCIXM
ID47   MGPPPTHIKYLHLNIYCNGKSTAPGIRSHSLGFALLSLSHPTCQA
ID48   MFCLLTFLAFTTLLFA
ID49   MHCGSTPGLCPCWVPFLKCLLAVLSSLFA
ID50   MNLVCSALLLLGIVSS
ID51   MSVLDDRQRDILVVQKRHSSLEAAMLIGLLAWLQT
ID52   MGVNGRRLLIICHYLPLSLC
ID53   MKLRECPALRWSQLSQHKLECLLLYLAESSG
ID54   MDPRGILKAFPKRQKIHADASSKVLAKIPRREEGEEAEEWLSSLRAHVVRTGIGRARAEL
              FEKQIVQHGGQLCPAQGPGVTHIVVDEGMDYERALRLLRLPQLPPXCSA
ID55   MFWKLSLSLFLVAVLVKVAEA
ID56   MAFLGLFSLLVLQSMATG
ID57   MAFLGLFSLLVLQSMATG
ID58   MSFSLNFTLPANTTSSPVTGGKETDCGPSLGLAAGIPLLVATALLVALLFTLIHR
ID59   MSTWYLALNKSYKNKDSVRIYLSLCTVSIKFTYFHDIQTNCLTTWKHSRCRFYWAFGGSI
              LQHSVDPLVLFLSLALLVTP
ID60   MAIGISLQLLCCIFTLVLQ
ID61   MQATSNLLNLLLLSLFAGL
ID62   MMKWKPEDLGSVPCEAFSVTLLCGWPGSHWC
ID63   MQATSNLLNLLLLSLFAGL
ID64   MASSHWNETTTSVYQYLGFQVQKIYPFHDNWNTACFVILLLFIFTVVS
ID65   MLWFSGVGALAERYCRRSPGITCCVLLLLNCSG
ID66   MLFLQMGKQSWTLIFFLNVTQLVRG
ID67   MELRXXPPGGREVQLLLGLCSPPXXSL
ID68   MLWSLLSSSGSHFG
ID69   MDISGLIPGLVSTFILLSXSDHYGRKFPMILSSVGALATSVWLCLLCYFAFP
ID70   MXVFFSKNRFEMYFSLLLFVILLITSLIFC
ID71   MPVPACWISSSLSLLASHHSVSC
ID72   MCPVFSKQLLACGSLLPGLWQ
ID73   MALTIHGERMRPDWESPWITSSQAQSLSLGGSPSSRGPLVPRGEYLASCPEGVRSHSHLL
              PRSLLPLSAWPPWAWH
ID74   MAARFRCGHLCVPEVPRGPASHAEGGGGRLSRKAAHQAQLCWRAGGDGRGNFN
              PMNFLVAGTFASSCHSPPLLWSLPPRILIASSLPTLSHP
ID75   MASTISAYKEKMKELSVLSLICSCFYTQP
ID76   MLQVYGKPVYQGHRSTLKKGPYLRFNSPSPKSRPQRPKVIERVKGTKVKSIRTQTDFYAT
              KPKKMDSKMKHSVPVLPHGDQQYLFSPSREMPTFSGTLEGHLIPMAILLGQTQS
ID77   MSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQATDLEQLTAHSASEL
              YVIAFGSNEDVIVLSMVIISFVVRVSLVWIFFFLLCVAERTYKQRLLFAKLFGHLTSA

SEQ. ID NO.	SIGNAL PEPTIDE
ID78	MCKGIKAGDTCEKLVGYSAVYRVCFGMACFFFIFCLLTLKINNSKSCRAHIHNGFWFFKL LLLGAMCSG
ID79	MSDSAGGRAGLRRYPKLPVWVVEDHQEVLPFIYRAIGSKHLPASNVSFLHFDSHPDLLIP VNMPADTVFDKETLFGELSIENWIMPAVYAGHFSHVVWFHPTWA
ID80	MSSCRGQKVAGGLRVVSPFPLCQPAGEPSRGKMRSSCVLLTALVALA
ID81	MIIPFKIKNLGGRVLLSGREMFPASVRAPDLAVALSLLPAWT
ID82	MVCSAPRKIVVRAFITIIFIYYAIKKRANEPAAYLMLKPEALILLLLAQKGPS
ID83	MTESSMKKLASTLLDAITDKDPLVQEQVCSALCSLGEVRP
ID84	MQETDCNKRWGRGLGGLWSETGRRFHCKSFVFLFHCTSGLSSC
ID85	MLLEVPWLSSTVSCAQG
ID86	MSGGRMQARCSQQSTWSPAFLAVAGPGWA
ID87	MLQMLWHFLASFFPRAGC
ID88	MYSHPVSSLVCLLAMGKGLG
ID89	MGRKEEDDCSXWKKQTTNIRKTFIFMEVLGSGAFS
ID90	MMIAVFGNANDRNVLTLLPNQSLFSLARA
ID91	MFFELPLVVTAWFFGMCRS
ID92	MNHNIIICVMYIVPFLMTKCLYFCHSCKRGSFLLIVANVHFSQT
ID93	MSCGSAASLTGLCXCCLQALG
ID94	MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLA
ID95	MAAAMXLLCSSCCSWGPAAG
ID96	MDFIKDQSLSHRSVVKVLSLRKAQA
ID97	MTRPFWASCSTWATSRISCAFSLASSTA
ID98	MKSCAVSLTTAAVAFG
ID99	MSIHECACLSLSLICLRMSLS
ID100	MLSGLSFLSVFSLWC
ID101	MGLKDKSQAPASGLGVLRGQRSGSFISMPAPASGQXPEESRSPAPPVASRSQNRGYRPWH GPLWVHQSVRFGLYSILHFPFWVHG
ID102	MSDQIKFIMDSLNKEPFRKNYNLITFDSLEPMQLLQVLSDVLA
ID103	MSPSCLHPDLWSMCLEVPSFTATDSVNCGCCLELATEPARNIRSTTRASLLRCSSFTSTR NSTGISALPPAAPMAWPFSASLSTLPVPLTHSSVASLTATPSLA
ID104	MDLSFHLLLDPSSTQS
ID105	MPHFLDWFVXVYLVISVLILVGFGAC
ID106	MSKLKVIPEKSLTNNSRJVGLLAQLEKINA
ID107	MMSASRLAGTLIPAMAFLSCVRP
ID108	MVDGTQLRGLTRMYQVPLXLDRDETLVRLRFTMVALVTVCCXLVAFLFC
ID109	MKQNFLVLNSVWYLISMLQMLAVIT
ID110	MECQNSSLKKCLLVEKSLVKASYLIAFQTAASKKPFSIAEELIKPYLVEMCLEVLGSSA
ID111	MHSSIKTKGSVMWLVALLEMCVC
ID112	MTVLPLEAISSLSSFVLG
ID113	MGTASRSNIARHLQTNLILFCVGAVGACTL
ID114	MNSSKEEMRELAALFYSVVVSTVSG
ID115	MSQDGGXGELKHMVMSFRVSELQVLLGFAGRNKSGRKHELLAKALHLLKSSC
ID116	MPCISLLGLLYNFVQVLCYLSIFCLGVLF
ID117	MKIAVLFCFFLLIIF
ID118	MAKQKPHVLGSRVMPASCVSERRRKPSFQVSTWSSASLRGSWQ
ID119	MGFLYLKSVFDVSLG
ID120	MRMGPGRKRDFSPVPWSQYFESMEDVEVENETGKDTFRVYKSGSEGPVLLLLHGGG HSALS
ID121	MIFLLYLLPSSEE
ID122	MRMGPGRKRDFSPVPWSQYFESMEDVEVENETGKDTFRVYKSGSEGPVLLLLHGGG HSALS

SEQ. ID NO.	SIGNAL PEPTIDE
ID123	MLSLLNLISILASIPS
ID124	MGTTSNMVTTIHLMLLWPVHPLLVG
ID125	MGDPERPEAAGLDQDERSSSDTNESEIKSNEEPLLRKSSRRFVIFPIQYPDIWKMYKQAQ ASFWTAEEVDLSKDLPHWNKLKADEKYFISHILAFFAASDG
ID126	MDAGLFSLLPHPPCVG
ID127	MLITLTYLIQGESA
ID128	MYTGFRIEATLLTRVQCLCAIPFAFS
ID129	MYKQAQASFWTAEEVDLSKDLPHWNKLKADEKYFISHILAFFAASDG
ID130	MLLHLCSVKNLYQNRFLGLAAMASPSRN
ID131	MPCPTWTCLKSFPSPTSS
ID132	MEDLFSPSIXPPAPNISVPILLGWGLNLTLGQG
ID133	MAETKDAAQMLVTFKDVAVTFTREEWRQLDLAQRTLYREVMLETCGLLVSLG
ID134	MLILSQNIAQLEA
ID135	MLLGASAQGLWAHSWTCSCSA
ID136	MAAPLELSCWGGGWG
ID137	MSXVGIDLGFLNCYIAVARS
ID138	MEYSKXFVVFSTMFTASSP
ID139	MPMASSPPPSPHPQEPAPLLPSLPRLSLPFRLPWASTATA
ID140	MQHVXGHXPDPIAIMYVCPPCGHTTWALGLKFLSSSSQ
ID141	MGWEMTCIKSFFWARSHAGFLKCLLLSSLQ
ID142	MVFGGVCPSVTSIIAESLQGWNLVQLSFAATTPVLA
ID143	MHFITWSLLFLYQCSL
ID144	MSGASPIERTPMEEAPSSCPTSSCWPSVASPSSSWS
ID145	MEWAGKQRDFQVRAAPGWDHLASFPGPSLRLFSGSQA
ID146	MIAFFDEDNPRKRRSYSFTQSAGILCQETTYSTPHTKLEKAKSPTADAKVVSLSLQTSSA
ID147	MGKSIXSLCSVXLKARLKGXLEAVHLCLRAQKRRTALFCTLPCPVERG
ID148	MCLHMTLFRVPFTFS
ID149	MLNILKTLTSAALP
ID150	MRARVWPRSHGIPVPSFLSKSSLSHTPSPLLCLYHPPVYT
ID151	MWNAVAIICNGSWCQTXSTSGLESLCLSLLIPGPKP
ID152	MLRLGLFKISWARC
ID153	MPFAEDKTYKYICRNFSNFCNVDVVEILPYLPCLTA
ID154	MPGSSGLRFICKSRNHPQFGSFSGTDSLSFLPPCPC
ID155	MDVTGDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKNPPGMDDQLXLVMEFCGAGS
ID156	MIFGLYFVLAVKLFLVFLLNICKG
ID157	MRKKRVEELIVFPGEVTSFSSIKCSSWISSLASG
ID158	MPSSSLAELCLMQQDACLFSXFLAVSRH
ID159	MDLWSCLFPVMLMEPSKGLEDSEWKMALQMRMQLPCLVLG
ID160	MSGKGKCRPIALRRAVPLPTTSTLTSA
ID161	MTPKAIQKSSGLFCPSQA
ID162	MPDQFDQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPEDV RGKCTSLLQLYDASNS
ID163	MCLVSFFLELNVLQQ
ID164	MRSLACLTPCGHA
ID165	MHLLSNWANPASS
ID166	MWSGKWALVSPFAMLHSVWRLIPA
ID167	MKVHMHTKFCLICLLTFIFH
ID168	MGRRHWVLTHSALSLFYTADTSHG
ID169	MAVFVVLLALVAGVLG
ID170	MAPLLLQLAVLGAALA

SEQ. ID NO.	SIGNAL PEPTIDE
ID171	MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVA
ID172	MELVLVFLCSLLAPMVLA
ID173	MGPIWSSYYGNCRSLLFVMDASDPTQLSASCVQLLGLLSAEQLAEA
ID174	MSGGRAPAVLLGGVASLLLSFVWMPALLPVASRLLLLPRVLLTMASG
ID175	MALSCTLNRYLLLMAQEHLEFRLPEIXSLLLLFGGQFASS
ID176	MAARGVIAPVGESLRYAEYLQPSAKRPDADVDQQRLVRSLIAVGLGVAALAFA
ID177	MRMCAGSIYKSATQAVLGXLFLGGLCRG
ID178	MAERRRPLSPIPSXRRPSEPSRPRPAAAGXRSLPRPGDEELQLPCAVHDLIFWRDVKKTG FVFGTTLIMLLSWQLSVS
ID179	MAAPVLLRVSVPRWERVARYAVCAAGILLSIYAYHVEREKERDPEHRALCDLGPWVK CSAALASRWGRGFGLLGSIFGKDGVLNQPNSVFGLIFYILQLLLGMTASAVA
ID180	MSFLQDPSFFTMGMWSIGAGALGAAALALLLANT
ID181	MASLLCCGPKLAACGIVLSAWGVIMLIMLGIFFNVHS
ID182	MILPYRMXSLFLHAVSSSFT
ID183	MATLVELPDSVLLEIFSYLPVRDRIRISRVCHRWKRLVDDRWLWRHVDLTLYTVRALAGR AWA
ID184	MKNACIVLPPTPPPSLQPSASLLAPNRFLFSCFCFLSHKFG
ID185	MAFGLQMFIQRKFPYPLQWSLLVAVVAG
ID186	MYCKILVLMLHTELIRTDYSSVDQLLLNYPAEEGLGRERSLLWTPLLSPGSLR
ID187	MAVSHSVKERTISENSLIILLQGLQG
ID188	MESGGRPSLCQFILLGTTSVVTA
ID189	MAALDLRAXWIRWSCSCLGXLXGAGGETNGVERPGGGGLALARQGSLRDGRQVGR APAVCFPHGAPGLPPRQRXXGGXPEVQGGESWCPRPRGGGASRTGLRRRKGPTKTPE PESSEAPQDPLNWFGILVPHSLRQAQA
ID190	MAFLPSPAWWISLLPSLLSIC
ID191	MEPKVAELKQKIEDTLCPFGFEVYPFQVAWYNELLPPAFHLPLPGPTLA
ID192	MLVLRSGLTKALA
ID193	MSGGHLADLTLLFVLLLFSLLPA
ID194	MKPSRTPARLWMLPQQQAGAVVVAAPTERHPTHHMAGWLLGALTLLGLVTS
ID195	MGESIPLAAPVPVEQAVLETFFSHLGIFSYDKAKDNVEKEREANKSAGGSWLSLLAALAH LAAA
ID196	MQMSYAIRCAFYQLLLAALMLVAMLQLLYLSLLSGLHG
ID197	MLRAELKIAVVLFAFHLLLSFILG
ID198	MNHQQTLIGRLLCDLHGLSLSPPVANNVQALFRMLTPEAYSCLLILLLRTFLCSA
ID199	MIITAVVSISVTIFCFQTKVDFTSCTGLFCVLGIVLLVTG
ID200	MAAGGRMEDGSLDITQSIEDDPLLDAQLLPHHSLQAHFRPRFHPLPTVIIVNLLWFIHLV FVVLX
ID201	MSPGCMLLFVFGFVGG
ID202	MKLLLGIALLAYVAS
ID203	MDILVPLLQLLVLLLTLPLHLMA
ID204	MEAASPSNSTGVERXADLMDADSLLLSLELASGSG
ID205	MIRQERSTSYQEAVRPALPSSKPCLLTSPAVLVKLLSSSASTS
ID206	MKLIDYGLSGYQEESAEVKAMDFITSTAILPLLFGCLGVFG
ID207	MRCLTTPMLLRALAQAARA
ID208	MSRFLNVLRSWLVMVSIIAMGNTLQSFRDHTFLYEKLYTGKPNLVNGLQARTFGIWTLLS SVIRCLC
ID209	MIFLTLSLDSRVSA
ID210	MQCFSFIKTMMILFNLLIFLCGAALLXVG
ID211	MAEAALEAVRXSYENSRPLQGSSACLLLCPTWTNP
ID212	MATASPSVFLLMVNGQVES
ID213	MAGIKALISLSFGGAIGLMFLMLGCALP

SEQ. ID NO.	SIGNAL PEPTIDE
ID214	MIGDILLFGTLLMNAGA
ID215	MKTMILTLSLFGSCIS
ID216	MDWRVPPSXXDPGHQDIPLPVTXXFISVSVLSSLGIVLA
ID217	MAAAALPAWLSLQSRA
ID218	MAMVSAMSWVLYLWISACAMLLCHG
ID219	MGKEWGWQEMENGGAAPAWGAGPPVHPAPPPVEKTLSWGCGFGLHSGFGGSGGG VGLCRLLCLVRLFCC
ID220	MLQTSNYSLVLSLQFLLLSYD
ID221	MWFEILPGLSVMGVCLLIPGLATA
ID222	MRPSPLSGILADPLXLFPFSEG
ID223	MRESLSXRSWHLPASLMMAQXFIPAVA
ID224	MSGVVPTAPEQPAXEMENQTKPPDPRPDAPPEYSSHXFTRTPWKQLSLHLLATRACYG
ID225	MWRYQFGWGVITRGPREIPFPPSLLASESLLPPLPDLVLTCTSLGFVTRVWMSLNLNELS LYSRTWVFTCLVFFCFG
ID226	MVKLLVAKILCMVGVFFFMLLGSLLPVKI
ID227	MPVSIMCLIGLKANASS
ID228	MKVILLYLVLEKLVSRA
ID229	MAVTLSLLLGGRVCXPSLA
ID230	MLNQTSGRTSLLPELGVVTPAQG
ID231	MTSENLVQTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVSAWKDL FVPRPVLRALSFLGFSAPTPIQA
ID232	MAAFGRQXXXWHXLIPLTWACMA
ID233	MSLTSSPKKRRSICFDRFLMPQSQSGPSSLGESYRTGVGFLIPEGWFLSGCPHGSSA
ID234	MGELGNRSRCILFLSENPCLSESIFQSLXFCLSPPPSPS
ID235	MAELGLNEHHQNEVINYMRFARSKRGLRLKTVDSCFQDLKESRLVEDTFTIDEVSEVLNG LQAVVHSEVESELINTAYTNVLLLRQXFAQAEK
ID236	MVTLPSGTWAFSCPYLALVDGGMLGSAREDAHASVVSWAVGLLYAVAQG
ID237	MASASARGNQDKDAHFPPPSKQSLLFCPKXXLHIHRAEISKIMRECQEESFWKRALPFSL VSMLVTQG
ID238	MLLMKSILLKVVCVLCIYLKFKLMALIYVPDKNNTNNNILRYNHNEISIGISVQCHFILS LCVLCIVLT
ID239	MAQRLLLRRFLASVIS
ID240	MAASKVKQDMPPXGGYGPIDYKRNLPRRGLSGYSMLAIGIGTLIYGHWSIMKWNRERRRL QIEDFEARIALLPLLQA
ID241	MRHLVTEELFPCSNLEDVVEDNSHSYFTLRITMACKGVPSTLLSLAILSHISTP
ID242	MSAEVKVTGQNQEQFLLLAKSAKGAALATLIHQVLEAPGVYVFGELLDMPNVRELAESXF ASTFRLLXVFAYGTYA
ID243	MLLSIGMLMLSATQVXTILXVQLFAFLNLLPVEA
ID244	MGWEVVSLSYCGVSWG
ID245	MRECISVHVGQAGVQIGNACWELFCLEHGIQA
ID246	MAGPLQGGGARALDLLRGLPRVSLA
ID247	MPAGVPMSTYLKMFAASXLAMCAGA
ID248	MAVQCVRLARRSLPALALSLRASP
ID249	MFSIISRSRACSMYFKENAKPSQLRLMHHYLSTPTSA
ID250	MKRLLPATSLAGPVLS
ID251	MLIITNPWPKYFDAAGRLTPEFSQRLTNKIRELLQQMERGLKSADXXDGTGYTGWAGIAV LYLHLYDVFG
ID252	MCATETVRAWLAQGSSSAGWG
ID253	MLLLATHPETVGQVTLRVXPVSLEVSIQMCAAAAAAFCLKXXGANT
ID254	MAASSATPAPXXSQRCGADAGSAARIVFRWGRGRRGARSPEGSGHHGRANSGLGGAQ LQGGAXG

SEQ. ID NO.	SIGNAL PEPTIDE
ID255	MLRRPLAGLAAAALGRA
ID256	MDRPGFVAALVAGGVAG
ID257	MIVWFEGISMDLLTLLFQRRS
ID258	MRTFVHFALDALMFPARRRA
ID259	MAAPPQLRALLVVVNALLRKRRYHAALAVLKGFRNGAVYGAKIRAPHALVMTFLFR NGSLQ
ID260	MPVDLGXALGLLPSLAKA
ID261	MNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAISATFKMLESSSQKFLQGLVYLIGNL MGLALAVYKCQS
ID262	MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIG
ID263	MAASGAPRILVDLLKLXVAPLAVFQMLKSMCAG
ID264	MASVSSATFSGHGARSLLQFLRLVGQ
ID265	MWYLAVLLVLFTLNIL
ID266	MFTFGRLFQIITVVTCLQFIQDCCIHSRQINSLLEXSSLSRC
ID267	MIQDRDRCAQAAAVAAVGNLEPRGTPGPEDEAFCLPGCVGTLCQLDWWIWG
ID268	MKIIFPILSNPVFRRTVKLLLCLLWIGYSQG
ID269	MVSRMVSTMLSGLLFWLASGWTPAFA
ID270	MTATLAAAADIATMVSGSSGLAXA

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Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3.5	0.121	0.036	0.467	0.664
4	0.096	0.06	0.519	0.708
4.5	0.078	0.079	0.565	0.745
5	0.062	0.098	0.615	0.782
5.5	0.05	0.127	0.659	0.813
6	0.04	0.163	0.694	0.836
6.5	0.033	0.202	0.725	0.855
7	0.025	0.248	0.763	0.878
7.5	0.021	0.304	0.78	0.889
8	0.015	0.368	0.816	0.909
8.5	0.012	0.418	0.836	0.92
9	0.009	0.512	0.856	0.93
9.5	0.007	0.581	0.863	0.934
10	0.006	0.679	0.835	0.919

TABLE IV

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3.5	2674	947	599	23	150
4	2278	784	499	23	126
4.5	1943	647	425	22	112
5	1657	523	353	21	96
5.5	1417	419	307	19	80
6	1190	340	238	18	68
6.5	1035	280	186	18	60
7	893	219	161	15	48
7.5	753	173	132	12	36
8	636	133	101	11	29
8.5	543	104	83	8	26
9	456	81	63	6	24
9.5	364	57	48	6	18
10	303	47	35	6	15

TABLE V

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	16	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	55	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

TABLE VI

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter sequence P13H2 (546 bp):

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.983	9	TGTCAGTTG
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.980	11	AATAGAATTAG
S8_01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHAE47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETAE47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA
SRY_02	-41	-	0.951	12	TAAAACAAAACA
E2F_02	-33	+	0.957	8	TTTAGCGC
MZF1_01	-5	-	0.975	8	TGAGGGGA

Promoter sequence P15B4 (861bp) :

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCCTGGAA
STAT_01	-673	-	0.951	9	TTCCAGGAA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTTC
MZF1_01	-424	+	0.986	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

Promoter sequence P29B6 (555 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

TABLE VII

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CLAIMS

1.   A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 38-270 or comprising a sequence complementary thereto.

5   2.   The nucleic acid of Claim 1, wherein said nucleic acid is recombinant.

3.   A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary thereto.

4.   A purified or isolated nucleic acid comprising at least 15 consecutive bases of

10   one of the sequences of SEQ ID NOs: 38-270 or one of the sequences complementary thereto.

5.   The nucleic acid of Claim 4, wherein said nucleic acid is recombinant.

6.   A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-270 or one of the

15   sequences complementary to the sequences of SEQ ID NOs: 38-270.

7.   The nucleic acid of Claim 6, wherein said nucleic acid is recombinant.

8.   A purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-270.

20   9.   A purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-270 or having a sequence complementary thereto.

10.   A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 38-270 which encode a signal peptide.

11.   A purified or isolated polypeptides comprising a signal peptide encoded by

25   one of the sequences of SEQ ID NOs: 38-270.

12.   A vector encoding a fusion protein comprising a polypeptide and a signal peptide, said vector comprising a first nucleic acid encoding a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-270 operably linked to a second nucleic acid encoding a polypeptide.

30   13.   A method of directing the extracellular secretion of a polypeptide or the insertion of a polypetide into the membrane comprising the steps of:

obtaining a vector according to Claim 12; and

introducing said vector into a host cell such that said fusion protein is secreted into the extracellular environment of said host cell or inserted into the membrane of said host cell.

14.   A method of importing a polypeptide into a cell comprising contacting said cell with a fusion protein comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-270 operably linked to said polypeptide.

15.   A method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-270, comprising the steps of:

obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-270;

contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-270 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA;

identifying a cDNA which hybridizes to said detectable probe; and

isolating said cDNA which hybridizes to said probe.

16.   An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 15.

17.   The cDNA of Claim 16 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

18.   A method of making a cDNA comprising one of the sequences of SEQ ID NOs: 38-270, comprising the steps of:

contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

hybridizing said first primer to said polyA tail;

reverse transcribing said mRNA to make a first cDNA strand;

making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-270; and

isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

19.   An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 18.

20.   The cDNA of Claim 19 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

21.   The method of Claim 18, wherein the second cDNA strand is made by:

contacting said first cDNA strand with a first pair of primers, said first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-270 and a third primer having a sequence therein which is included within the sequence of said first primer;

performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product;

contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NO:s 38-270 , and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and

performing a second polymerase chain reaction, thereby generating a second PCR product.

22.   An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 21.

23.   The cDNA of Claim 22 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

24.   The method of Claim 18 wherein the second cDNA strand is made by:

contacting said first cDNA strand with a second primer comprising at least 15 consecutive nucleotides of the sequences of SEQ ID NOs: 38-270;

hybridizing said second primer to said first strand cDNA; and

extending said hybridized second primer to generate said second cDNA strand.

25.   An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-270 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 24.

5   26.   The cDNA of Claim 25, wherein said cDNA comprises the full protein coding sequence partially included in of one of the sequences of SEQ ID NOs: 38-270.

27.   A method of making a protein comprising one of the sequences of SEQ ID NO: 271-503, comprising the steps of:

obtaining a cDNA encoding the full protein sequence partially included in one of the

10   sequences of sequence of SEQ ID NO: 38-270;

inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;

introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and

15   isolating said protein.

28.   An isolated protein obtainable by the method of Claim 27.

29.   A method of obtaining a promoter DNA comprising the steps of:

obtaining DNAs located upstream of the nucleic acids of SEQ ID NO: 38-270 or the sequences complementary thereto;

20   screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and

isolating said DNA comprising said identified promoter.

30.   The method of Claim 29, wherein said obtaining step comprises chromosome walking from said nucleic acids of SEQ ID NO: 38-270 or sequences complementary thereto.

25   31.   The method of Claim 30, wherein said screening step comprises inserting said upstream sequences into a promoter reporter vector.

32.   The method of Claim 30, wherein said screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

30   33.   An isolated promoter obtainable by the method of Claim 32.

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34.   An isolated or purified protein comprising one of the sequences of SEQ ID
NO: 271-503.

35.   In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in
length, the improvement comprising inclusion in said array of at least one of the sequences of
5   SEQ ID NOs: 38-270, or one of the sequences complementary to the sequences of SEQ ID
NOs: 38-270, or a fragment thereof of at least 15 consecutive nucleotides.

36.   The array of Claim 35 including therein at least two of the sequences of SEQ
ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or
fragments thereof of at least 15 consecutive nucleotides.

10   37.   The array of Claim 35 including therein at least five of the sequences of SEQ
ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or
fragments thereof of at least 15 consecutive nucleotides.

Cap

5'

OHOH

mRNA   AAAAA 3'

1) Oxidation of the cap
2) Chemical ligation

N

5' Amino-containing tag   AAAAA 3'

3) Reverse transcription

N

5' Amino-containing tag   cDNA 1st strand   Primer   5'

3' RT tag   AAAAA 3'

4) Elimination of the mRNAs
5) Synthesis of the 2nd cDNA strand

5' Primer   cDNA 2nd strand   3'

3'   5'

Figure 1

Figure 2

3/4

Figure 3

4 / 4

Promoter P13H2

-517 .... +1 ↑ +29 .... 33-30-4-C4-PU

Promoter P15B4

-805 .... +1 ↑ +55 .... 33-27-1-E11-PU

Promoter P29B6

-500 .... +1 ↑ +55 ...... 33-46-4-F4-PU
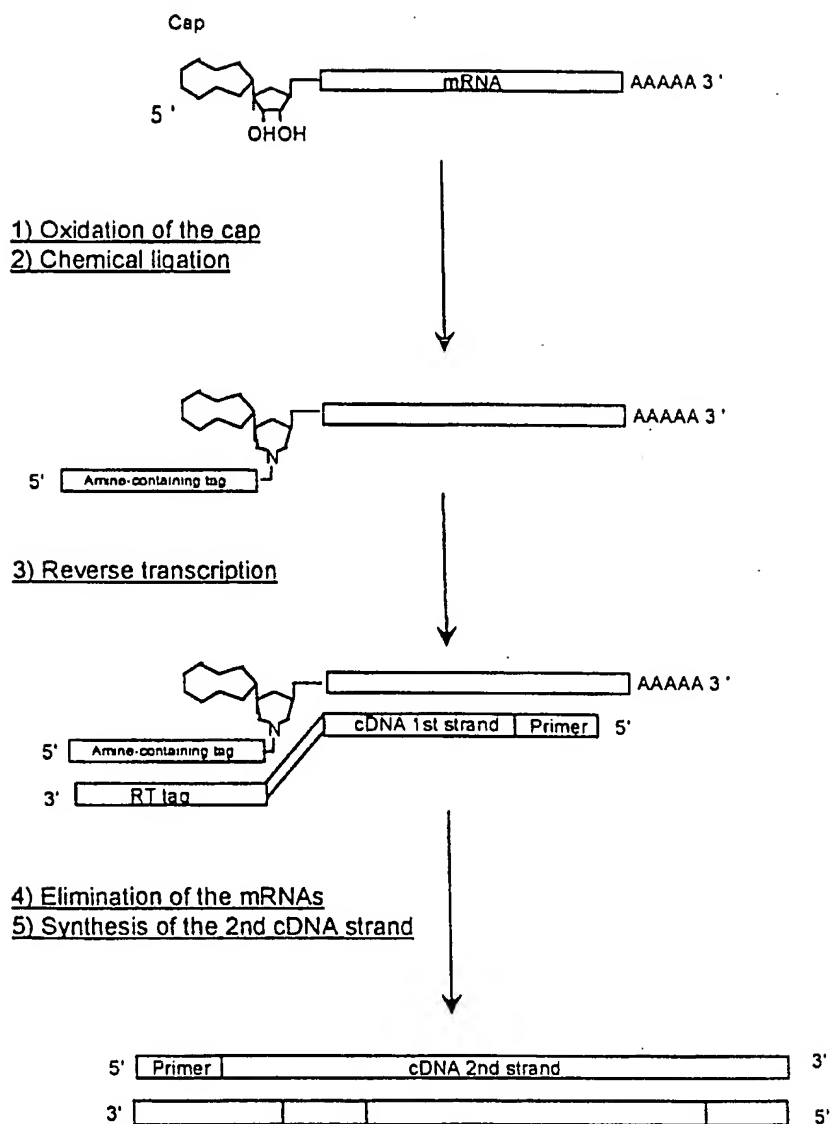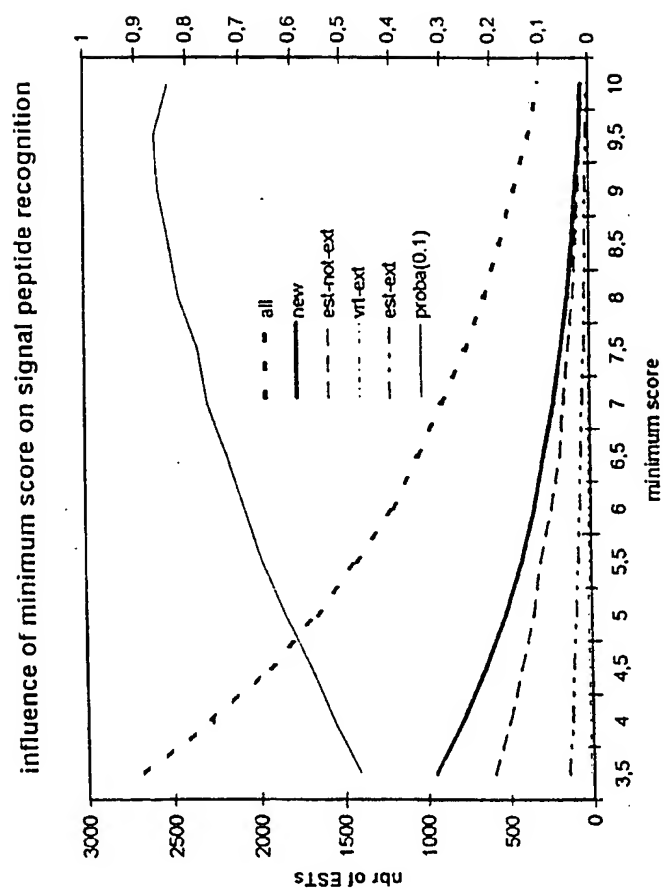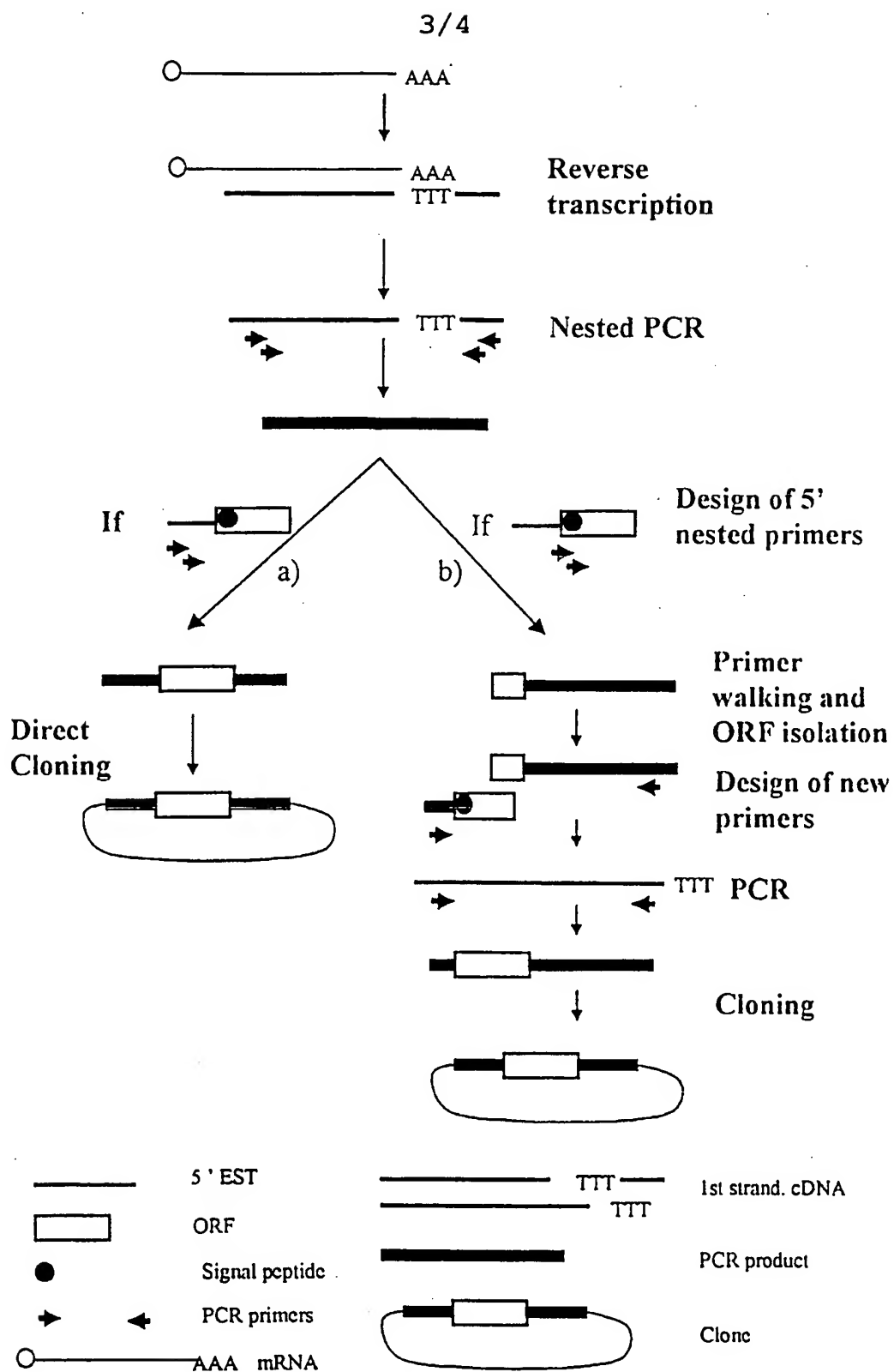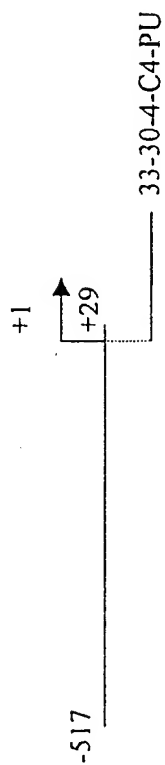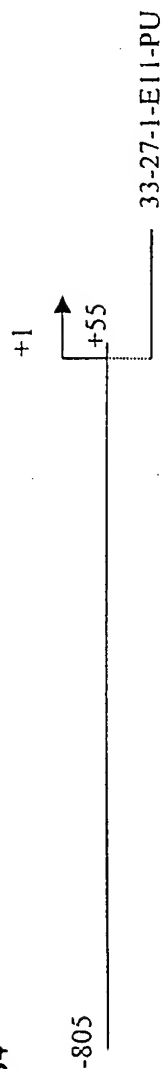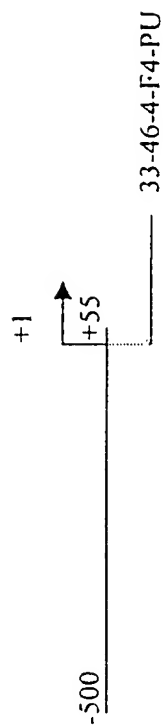
Figure 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
      (A) NAME : GENSET SA
      (B) STREET :24, RUE ROYALE
      (C) CITY: PARIS
      (E) COUNTRY : FRANCE
      (F) POSTAL CODE (ZIP) : 75008

    (ii) TITLE OF INVENTION: 5' EST FOR SECRETED PROTEINS EXPRESSED IN BRAIN

    (iii) NUMBER OF SEQUENCES: 503

    (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy Disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: Win95
      (D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 47 base pairs
      (B) TYPE: NUCLEIC ACID
      (C) STRANDEDNESS: SINGLE
      (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (ix) FEATURE:
      (A) NAME/KEY: Cap
      (B) LOCATION: 1
      (D) OTHER INFORMATION: m7Gppp added to 1

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UUCCACCCUA ACUCCUCCCA UCUCCAC   47

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 46 base pairs
      (B) TYPE: NUCLEIC ACID
      (C) STRANDEDNESS: SINGLE
      (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUAC CCCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCCAC   46

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCACGAGAC CATTA   25

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT   25

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC   25

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCAGTGGCTT AGGAG   25

(2) INFORMATION FOR SEQ ID NO: 7:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: SINGLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: Other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GCTACTTTGG ATGGC   25

(2) INFORMATION FOR SEQ ID NO: 8:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: SINGLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: Other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA   25

(2) INFORMATION FOR SEQ ID NO: 9:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: SINGLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: Other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGAATGG GAGACAAGCC AATTT   25

(2) INFORMATION FOR SEQ ID NO: 10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AAACAGCGTG AGTCC   25

(2) INFORMATION FOR SEQ ID NO: 11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA   25

(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG   25

(2) INFORMATION FOR SEQ ID NO: 13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CGCACGAGAC CATTA   25

(2) INFORMATION FOR SEQ ID NO: 14:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 67 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: SINGLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: Other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTT   60

TTTTTVN   67

(2) INFORMATION FOR SEQ ID NO: 15:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 29 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: SINGLE   ,
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: Other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG   29

(2) INFORMATION FOR SEQ ID NO: 16:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: SINGLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: Other nucleic acid

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG   25

(2) INFORMATION FOR SEQ ID NO: 17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 526 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Lymph ganglia

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(261..376)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 166..281
                                id N70479
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(380..486)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                region 54..160
                                id N70479
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(110..145)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                                region 403..438
                                id N70479
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(196..229)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                                region 315..348
                                id N70479
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 90..140
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.2
                                seq LLLITAILAVAVG/FP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATATRARAC AGCTACAATA TTCCAGGGCC ARTCACTTGC CATTTCTCAT AACAGCGTCA   60

```
GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTG ATC        113
                                  Met Lys Lys Val Leu Leu Leu Ile
                                      -15                     -10

ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TCT CAA GAC CAG        161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
            -5                  1                 5

GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR        209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
        10                  15                  20

WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT        257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
    25                  30                  35

CCA TTT CCA AGA TTT CCA TGG TTT AGA CGT AAN TTT CCT ATT CCA ATA        305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40                  45                  50                  55

CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA        354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                60                  65

GGAAAAGTCA CRATAAACCT GGTCACCTGA AATTGAAATT GAGCCACTTC CTTGAARAAT       414

CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA       474

GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA               526
```

(2) INFORMATION FOR SEQ ID NO: 18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 1..17
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.2
                         seq LLLITAILAVAVG/FP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 1               5                  10                  15

Gly
```

(2) INFORMATION FOR SEQ ID NO: 19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 822 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (D) DEVELOPMENTAL STAGE: Fetal
        (F) TISSUE TYPE: kidney

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 260..464
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                            region 153..357
                            id H57434
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 118..184
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                            region 98..164
                            id H57434
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 56..113
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                            region 35..92
                            id H57434
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 454..485
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                            region 348..379
                            id H57434
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 118..545
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                            region 1..428
                            id N27248
                            est

    (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 65..369
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 41..345
                                id H94779
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 61..399
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 6..344
                                id H09880
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 408..458
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 92
                                region 355..405
                                id H09880
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 60..399
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 56..395
                                id H29351
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 393..432
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 90
                                region 391..430
                                id H29351
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 346..408
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 5.5
                                seq SFLPSALVIWTSA/AF

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:


ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC      60

CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC     120

CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG     180

GTTTGTTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA      240
```

```
CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG    300

AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT    357
                                                 Met Trp Trp Phe
                                                 -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT    405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
    -15                 -10                 -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA    453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
    1               5               10                  15

GAC CCG GCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GCT CCA RAA    501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
                20                  25                  30

AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA    549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
            35                  40                  45

AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAAA          602
Lys

CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGTATT GCTTTCTACA CTGTTGAATT    662

GTCTGGCAAT ATTTCTGCAG TGGAAAATTT GATTTARMTA GTTCTTGACT GATAAATATG    722

GTAAGGTGGG CTTTTCCCCC TGTGTAATTG CTACTATGT CTTACTGAGC CAAGTTGTAW     782

TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA                          822
```

(2) INFORMATION FOR SEQ ID NO: 20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 1..21
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.5
                      seq SFLPSALVIWTSA/AF

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1               5               10                  15
```

Ile Trp Thr Ser Ala
       20

(2) INFORMATION FOR SEQ ID NO: 21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 405 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Testis

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(103..398)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                   region 1..296
                                   id AA442893
                                   est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 185..295
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.9
                                   seq LSYASSALSPCLT/AP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:


```
ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60

CCCAGCCCAA GTCAGCCTTC AGCACGCGCT TTTCTGCACA CAGATATTCC AGGCCTACCT     120

GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG     180

TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG     229
     Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
         -35             -30             -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC     277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
        -20             -15             -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GCT ATG ATG     325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
    -5               1               5               10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCARAAGGG   384
Pro Asp Asn
```

TTTCTAAAAA CAAAAAAAAA A   405

(2) INFORMATION FOR SEQ ID NO: 22:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 37 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 1..37
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 5.9
                                       seq LSYASSALSPCLT/AP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 1   5   10   15

Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
                20   25   30

Ser Pro Cys Leu Thr
            35

(2) INFORMATION FOR SEQ ID NO: 23:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 496 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Cancerous prostate

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 149..331
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 98
                                        region 1..183
                                        id AA397994
                                        est

        (ix) FEATURE:

         (A) NAME/KEY: other
         (B) LOCATION: 328..485
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION: identity 96
                                region 179..336
                                id AA397994
                                est

     (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: complement(182..496)
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION: identity 97
                                region 14..328
                                id AA399680
                                est

     (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 196..240
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 5.5
                                seq ILSTVTALTFAXA/LD

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AAAAAATTGG TCCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAG   60

ATTAGCCGTG GCCTAGGCCG TTTAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG   120

CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG   180

GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT   231
                 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
                 -15   -10   -5

GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT   279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
        1   5   10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG   327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
    15   20   25

GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT   375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
30   35   40   45

TCT TCA GCC TGAAATGAAK CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT   434
Ser Ser Ala

TGGAAAGTC AAATTGASCA TTATTAAATA AAGCTTGTTT AATATGTCTC AAACAAAAAA   494

AA   496

(2) INFORMATION FOR SEQ ID NO: 24:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 15 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR
                            .

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 1..15
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.5
                                seq ILSTVTALTFAXA/LD

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
 1   5   10   15

(2) INFORMATION FOR SEQ ID NO: 25:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 623 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Testis

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 49..96
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 10.1
                                seq LVLTLCTLPLAVA/SA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG   57
                                                        Met Glu Arg
                                                            -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT GCT GGC   105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
         -10   -5   1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG   153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
     5   10   15

```
GTC AGC AGC TGG ACG GAG TGC CCG CCC ACC TGG TGC AGC CCG CTG GAC        201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20            .          25                30          ,   .       35

CAA GTC TGC ATC TCC AAC GAG GTG GTC GTC TCT TTT AAA TGG AGT GTA        249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
                40                45                50

CGC GTC CTG CTC AGC AAA CGC TGT GCT CCC AGA TGT CCC AAC GAC AAC        297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
            55                60        .         65

ATG AAK TTC GAA TGG TCG CCG GCC CCC ATG GTG CAA GGC GTG ATC ACC        345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
            70                75  .              80

AGG CGC TGC TGT TCC TGG GCT CTC TGC AAC AGG GCA CTG ACC CCA CAG        393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
    85                90                95

GAG GGG CGC TGG GCC CTG CRA GGG GGG CTC CTG CTC CAG GAC CCT TCG        441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100               105               110               115

AGG GGC ARA AAA ACC TGG GTG CGG CCA CAG CTG GGG CTC CCA CTC TGC        489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
                120               125               130

CTT CCC AWT TCC AAC CCC CTC TGC CCA RGG GAA ACC CAG GAA GGA           534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
                135               140               145

TAACACTGTG GGTGCCCCCA CCTGTGCATT GGGACCACRA CTTCACCCTC TTGGARACAA      594

TAAACTCTCA TGCCCCCAAA AAAAAAAAA                                        623
```


    (2) INFORMATION FOR SEQ ID NO: 26:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 16 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 1..16
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 10.1
                            seq LVLTLCTLPLAVA/SA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala

1   5   10   15

(2) INFORMATION FOR SEQ ID NO: 27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 848 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (D) DEVELOPMENTAL STAGE: Fetal
        (F) TISSUE TYPE: kidney

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 32..73
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 10.7
                           seq LWLLFFLVTAIHA/EL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG   55
                                     Met Leu Trp Leu Leu Phe Phe Leu
                                                  -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT   103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
 -5   1   5   10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT   151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
            15   20   25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC   199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
         30   35   40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC   247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
        45   50   55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA   295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
        60   65   70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC   343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75   80   85   90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC   391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
            95   100   105

```
CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG      439
Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met
            110                 115                 120

GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC      487
Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys
            125                 130                 135

ATC ATC ATA GTT GCA ATT GCA CTA CTG ATT TTA TCA GGG ATC TGG CAA      535
Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln
            140                 145                 150

CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GTG GAT GAC GCT GAA RAT      583
Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa
155                 160                 165                 170

AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC      631
Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro
                175                 180                 185

CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT      679
Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp
                190                 195                 200

GAG AGG CTC ACC CCT CTC TGAAGGGCTG TTGTTCTGCT TCCTCAARAA            727
Glu Arg Leu Thr Pro Leu
                205

ATTAAACATT TGTTTCTGTG TGACTGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT    787

WTTTTGTTTC ACCATTCTTC TTTTGTAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA    847

C                                                                    848
```

(2) INFORMATION FOR SEQ ID NO: 28:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 1..14
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 10.7
                                  seq LWLLFFLVTAIHA/EL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```
Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 29:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: Other nucleic acid

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG   25

(2) INFORMATION FOR SEQ ID NO: 30:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 26 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: SINGLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: Other nucleic acid

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTC   26

(2) INFORMATION FOR SEQ ID NO: 31:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 546 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: Genomic DNA

     (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION: 1..517

     (ix) FEATURE:
          (A) NAME/KEY: transcription start site
          (B) LOCATION: 518

     (ix) FEATURE:
          (A) NAME/KEY: TF binding-site
          (B) LOCATION: 17..25
          (C) IDENTIFICATION METHOD: matinspector prediction
          (D) OTHER INFORMATION: name CMYB_01
                             score 0.983
                             sequence TGTCAGTTG

```
(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(18..27)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name MYOD_Q6
                              score 0.961
                              sequence CCCAACTGAC

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(75..85)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name S8_01
                              score 0.960
                              sequence AATAGAATTAG

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 94..104
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name S8_01
                              score 0.966
                              sequence AACTAAATTAG

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(129..139)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name DELTAEF1_01
                              score 0.960
                              sequence GCACACCTCAG

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(155..165)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name GATA_C
                              score 0.964
                              sequence AGATAAATCCA

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 170..178
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name CMYB_01
                              score 0.958
                              sequence CTTCAGTTG

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 176..189
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name GATA1_02
                              score 0.959
                              sequence TTGTAGATAGGACA

(ix)  FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 180..190
      (C) IDENTIFICATION METHOD: matinspector prediction
```

    (D) OTHER INFORMATION: name GATA_C
                              score 0.953
                              sequence AGATAGGACAT

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 284..299
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name TAL1ALPHAE47_01
                              score 0.973
                              sequence CATAACAGATGGTAAG

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 284..299
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name TAL1BETAE47_01
                              score 0.983
                              sequence CATAACAGATGGTAAG

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 284..299
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name TAL1BETAITF2_01
                              score 0.978
                              sequence CATAACAGATGGTAAG

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(287..296)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name MYOD_Q6
                              score 0.954
                              sequence ACCATCTGTT

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(302..314)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name GATA1_04
                              score 0.953
                              sequence TCAAGATAAAGTA

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 393..405
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name IK1_01
                              score 0.963
                              sequence AGTTGGGAATTCC

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 393..404
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name IK2_01
                              score 0.985
                              sequence AGTTGGGAATTC

(ix) FEATURE:

           (A) NAME/KEY: TF binding-site
           (B) LOCATION: 396..405
           (C) IDENTIFICATION METHOD: matinspector prediction
           (D) OTHER INFORMATION: name CREL_01
                                   score 0.962
                                   sequence TGGGAATTCC

     (ix) FEATURE:
           (A) NAME/KEY: TF binding-site
           (B) LOCATION: 423..436
           (C) IDENTIFICATION METHOD: matinspector prediction
           (D) OTHER INFORMATION: name GATA1_02
                                   score 0.950
                                   sequence TCAGTGATATGGCA

     (ix) FEATURE:
           (A) NAME/KEY: TF binding-site
           (B) LOCATION: complement(478..489)
           (C) IDENTIFICATION METHOD: matinspector prediction
           (D) OTHER INFORMATION: name SRY_02
                                   score 0.951
                                   sequence TAAAACAAAACA

     (ix) FEATURE:
           (A) NAME/KEY: TF binding-site
           (B) LOCATION: 486..493
           (C) IDENTIFICATION METHOD: matinspector prediction
           (D) OTHER INFORMATION: name E2F_02
                                   score 0.957
                                   sequence TTTAGCGC

     (ix) FEATURE:
           (A) NAME/KEY: TF binding-site
           (B) LOCATION: complement(514..521)
           (C) IDENTIFICATION METHOD: matinspector prediction
           (D) OTHER INFORMATION: name MZF1_01
                                   score 0.975
                                   sequence TGAGGGGA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGAGTGCAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCATTCAA ATCTTCTATG   60

TCTTGATTTG CCTGCTAATT CTATTATTTC TGGAACTAAA TTAGTTTGAT GGTTCTATTA   120

GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTTC TTCAGTTGTA   180

GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AGGGAGATCT TTTTTCCAAA   240

ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG   300

ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGAGAAGGGA AGAGGTCGTA   360

GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCCGTTCA TGTGATTTAG   420

CATCAGTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC AGAGGGTTAA AATTGTGTGT   480

TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGGTCCCCTC AAACAGATTC CCATGAATCT   540

CTTCAT   546

(2) INFORMATION FOR SEQ ID NO: 32:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: SINGLE
    (D) TOPOLOGY: LINEAR

  (ii) MOLECULE TYPE: Other nucleic acid

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACCAGGGA CTGTGACCAT TGC   23

(2) INFORMATION FOR SEQ ID NO: 33:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: SINGLE
    (D) TOPOLOGY: LINEAR

  (ii) MOLECULE TYPE: Other nucleic acid

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCCAAG AGAG   24

(2) INFORMATION FOR SEQ ID NO: 34:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 861 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: DOUBLE
    (D) TOPOLOGY: LINEAR

  (ii) MOLECULE TYPE: Genomic DNA

  (ix) FEATURE:
    (A) NAME/KEY: promoter
    (B) LOCATION: 1..806

  (ix) FEATURE:
    (A) NAME/KEY: transcription start site
    (B) LOCATION: 807

  (ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(60..70)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name NFY_Q6
            score 0.956

                              sequence GGACCAATCAT

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: 70..77
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name MZF1_01
                             score 0.962
                             sequence CCTGGGGA

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: 124..132
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name CMYB_01
                             score 0.994
                             sequence TGACCGTTG

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: complement(126..134)
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name VMYB_02
                             score 0.985
                             sequence TCCAACGGT

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: 135..143
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name STAT_01
                             score 0.968
                             sequence TTCCTGGAA

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: complement(135..143)
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name STAT_01
                             score 0.951
                             sequence TTCCAGGAA

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: complement(252..259)
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name MZF1_01
                             score 0.956
                             sequence TTGGGGGA

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: 357..368
     (C) IDENTIFICATION METHOD: matinspector prediction
     (D) OTHER INFORMATION: name IK2_01
                             score 0.965
                             sequence GAATGGGATTTC

(ix) FEATURE:
     (A) NAME/KEY: TF binding-site
     (B) LOCATION: 384..391

        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name MZF1_01
                        score 0.986
                        sequence AGAGGGGA

  (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: complement(410..421)
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name SRY_02
                        score 0.955
                        sequence GAAAACAAAACA

  (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: 592..599
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name MZF1_01
                        score 0.960
                        sequence GAAGGGGA

  (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: 618..627
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name MYOD_Q6
                        score 0.981
                        sequence AGCATCTGCC

  (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: 632..642
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name DELTAEF1_01
                        score 0.958
                        sequence TCCCACCTTCC

  (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: complement(813..823)
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name S8_01
                        score 0.992
                        sequence GAGGCAATTAT

  (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: complement(824..831)
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name MZF1_01
                        score 0.986
                        sequence AGAGGGGA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TACTATAGGG CACGCGTGGT CGACGGCCGG GCTGTTCTGG AGCAGAGGGC ATGTCAGTAA   60

TGATTGGTCC CTGGGGAAGG TCTGGCTGGC TCCAGCACAG TGAGGCATTT AGGTATCTCT   120

CGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGGT AGGGACAGGG   180

```
CTCAGAGGGC TAGGCACGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTGAGARG   240

GGAGCATGCC TTCCCCCAAC CCTGGCTTSC YCTTGGYMAM AGGGCGKTTY TGGGMACTTR   300

AAYTCAGGGC CCAASCAGAA SCACAGGCCC AKTCNTGGCT SMAAGCACAA TAGCCTGAAT   360

GGGATTTCAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGTTTT   420

CCAAATCAAG GTAACTTGCT CCCTTCTGCT ACGGGCCTTG GTCTTGGCTT GTCCTCACCC   480

AGTCGGAACT CCCTACCACT TTCAGGAGAG TGGTTTTAGG CCCGTGGGGC TGTTCTGTTC   540

CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG   600

TGGGTTCTCG CCCAAAGAGC ATCTGCCCAT TTCCCACCTT CCCTTCTCCC ACCAGAAGCT   660

TGCCTGAGCT GTTTGGACAA AAATCCAAAC CCCACTTGGC TACTCTGGCC TGGCTTCAGC   720

TTGGAACCCA ATACCTAGGC TTACAGGCCA TCCTGAGCCA GGGGCCTCTG GAAATTCTCT   780

TCCTGATGGT CCTTTAGGTT TGGGCACAAA ATATAATTGC CTCTCCCCTC TCCCATTTTC   840

TCTCTTGGGA GCAATGGTCA C                                            861
```

(2) INFORMATION FOR SEQ ID NO: 35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
CTGGGATGGA AGGCACGGTA                                               20
```

(2) INFORMATION FOR SEQ ID NO: 36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: SINGLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Other nucleic acid

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
GAGACCACAC AGCTAGACAA                                               20
```

(2) INFORMATION FOR SEQ ID NO: 37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 555 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: Genomic DNA

    (ix) FEATURE:
        (A) NAME/KEY: promoter
        (B) LOCATION: 1..500

    (ix) FEATURE:
        (A) NAME/KEY: transcription start site
        (B) LOCATION: 501

    (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: 191..206
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name ARNT_01
                        score 0.964
                        sequence GGACTCACGTGCTGCT

    (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: 193..204
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name NMYC_01
                        score 0.965
                        sequence ACTCACGTGCTG

    (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: 193..204
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name USF_01
                        score 0.985
                        sequence ACTCACGTGCTG

    (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: complement(193..204)
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name USF_01
                        score 0.985
                        sequence CAGCACGTGAGT

    (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: complement(193..204)
        (C) IDENTIFICATION METHOD: matinspector prediction
        (D) OTHER INFORMATION: name NMYC_01
                        score 0.956
                        sequence CAGCACGTGAGT

    (ix) FEATURE:
        (A) NAME/KEY: TF binding-site
        (B) LOCATION: complement(193..204)

.(C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name MYCMAX_02
                            score 0.972
                            sequence CAGCACGTGAGT

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 195..202
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name USF_C
                            score 0.997
                            sequence TCACGTGC

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(195..202)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name USF_C
                            score 0.991
                            sequence GCACGTGA

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(210..217)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name MZF1_01
                            score 0.968
                            sequence CATGGGGA

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 397..410
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name ELK1_02
                            score 0.963
                            sequence CTCTCCGGAAGCCT

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: 400..409
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name CETS1P54_01
                            score 0.974
                            sequence TCCGGAAGCC

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(460..470)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name AP1_Q4
                            score 0.963
                            sequence AGTGACTGAAC

(ix) FEATURE:
    (A) NAME/KEY: TF binding-site
    (B) LOCATION: complement(460..470)
    (C) IDENTIFICATION METHOD: matinspector prediction
    (D) OTHER INFORMATION: name AP1FJ_Q2
                            score 0.961
                            sequence AGTGACTGAAC

```
        (ix) FEATURE:
              (A) NAME/KEY: TF binding-site
              (B) LOCATION: 547..555
              (C) IDENTIFICATION METHOD: matinspector prediction
              (D) OTHER INFORMATION:  name PADS_C
                                      score 1.000
                                      sequence TGTGGTCTC

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
```

```
CTATAGGGCA CGCKTGGTCG ACGGCCCGGG CTGGTCTGGT CTGTKGTGGA GTCGGGTTGA      60

AGGACAGCAT TTGTKACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT     120

KAWAAGCTCA GCACCGGTGC CCATCACAGG GCCGGCAGCA CACACATCCC ATTACTCAGA     180

AGGAACTGAC GGACTCACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA     240

GAGCAGTCAG ACAGTGCCTG GGATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT     300

CATTCCTGTC TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG     360

GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAAATCACC     420

CGTGTCTTCT GCCTGCTCCC GCTCACATCC CACACTTGTG TTCAGTCACT GAGTTACAGA     480

TTTTGCCTCC TCAATTTCTC TTGTCTTAGT CCCATCCTCT GTTCCCCTGG CCAGTTTGTC     540

TAGCTGTGTG GTCTC                                                      555
```

```
(2) INFORMATION FOR SEQ ID NO: 38:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 155 base pairs
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: DOUBLE
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 45..86
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 10.8
                                      seq LLLLGLCLGLSLC/VG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
```

```
AGTGTCCCGC CGGGTCCCCG AGCGTCCCGC GCCCTCGCCC CGCC ATG CTC CTG CTG      56
                                                  Met Leu Leu Leu

CTG GGG CTG TGC CTG GGG CTG TCC CTG TGT GTG GGG TCG CAG GAA GAG     104
```

```
Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val Gly Ser Gln Glu Glu
-10               -5                  1                   5

GCG CAG AGC TGG GGC CAC TCT TCG GAG CAG GAT GGA CTC AGG GTC CCG    152
Ala Gln Ser Trp Gly His Ser Ser Glu Gln Asp Gly Leu Arg Val Pro
         10                  15                  20

AGG                                                                155
Arg
```

(2) INFORMATION FOR SEQ ID NO: 39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 427 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 191..268
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 10.8
                            seq VLLFFVLLGMSQA/GS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
AAGTACACGC GGMGAACTGG GAAGACAGAA AGWWCAATCC TTTAAGGGAG AACCTAGAAG    60

CCATTCAACA AGGTTAAAAT CTTTAGGCTT CCGAGGATTT GGTAGACAGA TCAGAGGCAC   120

GTTTCCCACA ACTGCGAAGA GGCGCTGAGG CAATTCTGCA AGAAGATTTT GGGGTTTTGG   180

AAAAGAAGCT ATG GAA AAC GGA GGG GCA GGC ACT CTG CAG ATA AGG CAA     229
            Met Glu Asn Gly Gly Ala Gly Thr Leu Gln Ile Arg Gln
                -25             -20                 -15

GTC CTG CTT TTC TTT GTT TTG CTG GGA ATG TCT CAG GCG GGC TCT GAA    277
Val Leu Leu Phe Phe Val Leu Leu Gly Met Ser Gln Ala Gly Ser Glu
         -10                  -5                  1

ACT GGG AAC TTT TTG GTG ATG GAG GAA TTG CAG AGC GGG AGC TTT GTA    325
Thr Gly Asn Phe Leu Val Met Glu Glu Leu Gln Ser Gly Ser Phe Val
    5                   10                  15

GGA AAT TTG GCA AAG ACC CTG GGA CTC GAG GTG AGT GAG CTG TCT TCG    373
Gly Asn Leu Ala Lys Thr Leu Gly Leu Glu Val Ser Glu Leu Ser Ser
20                  25                  30                  35

CGG GGG GCT CGG GTG GTT TCT AAT GAT AAC AAA GAG TGT TTG CAG CTG    421
Arg Gly Ala Arg Val Val Ser Asn Asp Asn Lys Glu Cys Leu Gln Leu
                40                  45                  50
```

GAC ACG   427
Asp Thr

(2) INFORMATION FOR SEQ ID NO: 40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 398 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 12..389
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 10
                         seq LKLLLFLSTELQA/SQ

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:


```
AAAAAAGGAC C ATG AGA GGG CCG GAG CCG GGT CCC CAA CCG ACG ATG GAG      50
             Met Arg Gly Pro Glu Pro Gly Pro Gln Pro Thr Met Glu
             -125             -120             -115

GGA GAC GTG CTG GAC ACA CTG GAG GCG CTG GGG TAT AAA GGA CCA TTG      98
Gly Asp Val Leu Asp Thr Leu Glu Ala Leu Gly Tyr Lys Gly Pro Leu
            -110             -105             -100

TTA GAA GAG CAA GCC CTT ACA AAG GCG GCA GAG GGT GGA TTA TCT TCA      146
Leu Glu Glu Gln Ala Leu Thr Lys Ala Ala Glu Gly Gly Leu Ser Ser
        -95             -90             -85

CCT GAA TTT TCA GAG CTC TGT ATT TGG TTA GGC TCT CAA ATA AAA TCA      194
Pro Glu Phe Ser Glu Leu Cys Ile Trp Leu Gly Ser Gln Ile Lys Ser
        -80             -75             -70

TTA TGC AAC TTG GAA GAA AGT ATC ACG TCT GCT GGA AGA GAT GAT CTA      242
Leu Cys Asn Leu Glu Glu Ser Ile Thr Ser Ala Gly Arg Asp Asp Leu
-65             -60             -55             -50

GAG AGC TTC CAG CTT GAG ATA AGT GGC TTT TTA AAA GAA ATG GCA TGT      290
Glu Ser Phe Gln Leu Glu Ile Ser Gly Phe Leu Lys Glu Met Ala Cys
            -45             -40             -35

CCA TAT TCT GTA CTC ATA TCA GGA GAT ATT AAA GAT CGT TTA AAA AAG      338
Pro Tyr Ser Val Leu Ile Ser Gly Asp Ile Lys Asp Arg Leu Lys Lys
            -30             -25             -20

AAG GAG GAC TGT TTG AAA CTT CTA TTA TTT TTA AGT ACA GAA CTT CAA      386
Lys Glu Asp Cys Leu Lys Leu Leu Leu Phe Leu Ser Thr Glu Leu Gln
        -15             -10             -5
```

```
GCT TCA CAG ATA                                                      398
Ala Ser Gln Ile
    1
```

(2) INFORMATION FOR SEQ ID NO: 41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 201 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 70..147
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 9.6
                              seq WLIALASWSWALC/RI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
AGCCCGGTTT CGTGCCCGCG GCCGACTGCG CASCTGTCCG CGAGTCTGAG ATACTTACAG    60

AGAGCTACA ATG GAA AAG TCC TGG ATG CTG TGG AAC TTT GTT GAA AGA TGG  111
          Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp
              -25             -20             -15

CTA ATA GCC TTG GCT TCA TGG TCT TGG GCT CTC TGC CGT ATT TCT CTT    159
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu
        -10             -5               1

TTA CCT TTA ATA GTG ACT TTT CAT CTG TAT GGA GGT TCG GGG            201
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ser Gly
 5               10              15
```

(2) INFORMATION FOR SEQ ID NO: 42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 272 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

(ix). FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 6..113
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 9.5
                             seq LGLLLLARHWCIA/GV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AGATT ATG CAG CAG ACT CGC ACA GAG GCT GTC GCG GGC GCG TTC TCT CAC   50
      Met Gln Gln Thr Arg Thr Glu Ala Val Ala Gly Ala Phe Ser His
        -35   -30   -25

TGC CTG GGC TTC TGT GGA ATG AGA CTC GGG CTC CTT CTA CTT GCA AGA   98
Cys Leu Gly Phe Cys Gly Met Arg Leu Gly Leu Leu Leu Leu Ala Arg
  -20   -15   -10

CAC TGG TGC ATT GCA GGT GTG TTT CCG CAG AAG TTT GAT GGT GAC AGT   146
His Trp Cys Ile Ala Gly Val Phe Pro Gln Lys Phe Asp Gly Asp Ser
  -5   1   5   10

GCC TAC GTG GGG ATG AGT GAC GGA AAC CCA GAG CTC CTG TCA ACC AGC   194
Ala Tyr Val Gly Met Ser Asp Gly Asn Pro Glu Leu Leu Ser Thr Ser
        15   20   25

CAG ACC TAC AAC GGC CAG AGC GAG AAC AAC GAA GAC TAT GAG ATC CCC   242
Gln Thr Tyr Asn Gly Gln Ser Glu Asn Asn Glu Asp Tyr Glu Ile Pro
      30   35   40

CCG ATA ACA CCT CCC AAC CTC CCG GAA GCG   272
Pro Ile Thr Pro Pro Asn Leu Pro Glu Ala
 45   50

(2) INFORMATION FOR SEQ ID NO: 43:

    (i) SEQUENCE CHARACTERISTICS:.
        (A) LENGTH: 186 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 28..99
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 9.1
                              seq LVVFLLLPLASGP/QV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATTTACGTCT TTTCAGTTTT TTTAGAG ATG GAA AAG GGA AAC GCG TTT TTA AAG   54

```
                              Met Glu Lys Gly Asn Ala Phe Leu Lys
                                                               -20

AAT AGG TTA GTT GTT TTT CTT CTC CTG CCC CTA GCA TCA GGA CCA CAG      102
Asn Arg Leu Val Val Phe Leu Leu Leu Pro Leu Ala Ser Gly Pro Gln
-15                 -10                 -5                   1

GTA AAA AGG AAA AGC GAA ATT ACG AAA CTT ATA AAG GCC ACG CGA ATC      150
Val Lys Arg Lys Ser Glu Ile Thr Lys Leu Ile Lys Ala Thr Arg Ile
            5                   10                  15

ATT TGT TTA TTC AAT AAA TTT AGT AGA GGA AAC GGG                      186
Ile Cys Leu Phe Asn Lys Phe Ser Arg Gly Asn Gly
        20                  25
```

(2) INFORMATION FOR SEQ ID NO: 44:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 400 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 164..235
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 9
                                    seq LLMLIVFHAASMA/LQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
AGTTAATTTG AACAAAATAT AGTAAGTATA CTATTATTTT CCATGTCTTT CTAGGCTTTT      60

TAAACTCTGC AGTGTATTTA CTGTACTCTC GTAGAAGGAG TGCCATCAAC TGCAATTGGT     120

ACAAATTGTG CTTATTTTTC TGCTCTTTTC ACGTTCCCAA AAT ATG TTC CCA TTC      175
                                                 Met Phe Pro Phe

AAC CAG GCA GGT CTT CCT ACT CTT CTC ATG CTC ATT GTT TTT CAT GCT      223
Asn Gln Ala Gly Leu Pro Thr Leu Leu Met Leu Ile Val Phe His Ala
-20                 -15                 -10                 -5

GCT TCC ATG GCT TTA CAG AGA CTC TTC CTC TTC GCT TTG GTC TGG CAT      271
Ala Ser Met Ala Leu Gln Arg Leu Phe Leu Phe Ala Leu Val Trp His
                1                   5                   10

TCA AAA CCC TCA GGA CTG ATG ACA GGC AAA CTA GAA TCT CAA ATT CCC      319
Ser Lys Pro Ser Gly Leu Met Thr Gly Lys Leu Glu Ser Gln Ile Pro
            15                  20                  25

CAT GAA AAG TTG ACT CAT ATC TCT GTC ATG CAT GGT CCC CTC AGT TCC      367
```

His Glu Lys Leu Thr His Ile Ser Val Met His Gly Pro Leu Ser Ser
    30   35   40

CAT CAC TCA TAC ACT CAC ATA CAT TTA TTT TTA   400
His His Ser Tyr Thr His Ile His Leu Phe Leu
45   50   55

(2) INFORMATION FOR SEQ ID NO: 45:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 297 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 1..228
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.8
                                    seq SLLLWMSSLPSLG/EK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG ACT TCA CGT AGC TTG CGT CGC TGC TCC TGT CTC CGT GTA ACT CAC   48
Met Thr Ser Arg Ser Leu Arg Arg Cys Ser Cys Leu Arg Val Thr His
    -75   -70   -65

AAT AAA GAG ATT TTG GCA TCA ACC GTG AGC TTA GGG GTA GAA GGG TAT   96
Asn Lys Glu Ile Leu Ala Ser Thr Val Ser Leu Gly Val Glu Gly Tyr
-60   -55   -50   -45

ATG TTA GGA GGT GGG AGC AGA ATC AAT TCT TCA AAT CTT AAT GAT GGT   144
Met Leu Gly Gly Gly Ser Arg Ile Asn Ser Ser Asn Leu Asn Asp Gly
            -40   -35   -30

GAA GAA GAG TGC TCA CCA GAT TCC CTT CTG GTC TGG AAA AAG AAA TCC   192
Glu Glu Glu Cys Ser Pro Asp Ser Leu Leu Val Trp Lys Lys Lys Ser
            -25   -20   -15

CTT CTT TTG TGG ATG TCA TCT CTA CCA TCT CTC GGT GAA AAA TAT TTC   240
Leu Leu Leu Trp Met Ser Ser Leu Pro Ser Leu Gly Glu Lys Tyr Phe
        -10   -5   1

AAG AGA ATT CTA AGA TGG AGA GAG CAT TGG AAG TCA TCC GGC CCA ATT   288
Lys Arg Ile Leu Arg Trp Arg Glu His Trp Lys Ser Ser Gly Pro Ile
5   10   15   20

CCC TTG TGG   297
Pro Leu Trp

(2) INFORMATION FOR SEQ ID NO: 46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 213 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 10..168
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.8
                        seq ILLLLTVLPCIXM/GQ

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
AACTGTAGC ATG TGG ACA GCC AGT GCC ATG GAT TTC AGA ACC TGC ATT GCC   51
          Met Trp Thr Ala Ser Ala Met Asp Phe Arg Thr Cys Ile Ala
              -50             -45                 -40

AGT KGA CTG CCT GCT TTG TGC TAC GTG CAG GCC TGC CGC GCC CTG ATG   99
Ser Xaa Leu Pro Ala Leu Cys Tyr Val Gln Ala Cys Arg Ala Leu Met
            -35             -30             -25

ATT GCT GCC TCG GTC CTG GGT CTG CCG GCC ATT TTA CTG CTG CTG ACT   147
Ile Ala Ala Ser Val Leu Gly Leu Pro Ala Ile Leu Leu Leu Leu Thr
            -20             -15             -10

GTT CTT CCC TGC ATC SGG ATG GGC CAG GAG CCC GGT GTG GCT AAG TAC   195
Val Leu Pro Cys Ile Xaa Met Gly Gln Glu Pro Gly Val Ala Lys Tyr
        -5              1               5

AGG SGG GCC CAG CTG GCT                                           213
Arg Xaa Ala Gln Leu Ala
10              15
```

(2) INFORMATION FOR SEQ ID NO: 47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 319 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

(ix).FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 62..196
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.5
                                seq FALLSLSHPTCQA/GA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATTGGTGCAG AGGCCCTTCT TGTCTCCACA CCAGAAGGAG CTGAGCAGAG GGGCCACAGC   60

G ATG GGA CCC CCT CCA ACC CAC ATT AAA TAC CTC CAC CTG AAT ATT TAT   109
  Met Gly Pro Pro Pro Thr His Ile Lys Tyr Leu His Leu Asn Ile Tyr
  -45   -40   -35   -30

TGC AAC GGC AAG AGC ACT GCA CCT GGA ATC CGG TCT CAC AGC CTT GGA   157
Cys Asn Gly Lys Ser Thr Ala Pro Gly Ile Arg Ser His Ser Leu Gly
                -25   -20   -15

TTT GCC TTG CTA AGC CTC AGT CAT CCA ACC TGC CAG GCA GGT GCA CCT   205
Phe Ala Leu Leu Ser Leu Ser His Pro Thr Cys Gln Ala Gly Ala Pro
            -10   -5   1

GCC GCA GCC CTG CCT TCT CTG TGG AGC TGG TGC TCT CGG GGT GCA CGA   253
Ala Ala Ala Leu Pro Ser Leu Trp Ser Trp Cys Ser Arg Gly Ala Arg
    5   10   15

GTC AGG GTT GGG AGG ATG CTT TCT CAC CTG TAC ACC TGT GGA TGG TAC   301
Val Arg Val Gly Arg Met Leu Ser His Leu Tyr Thr Cys Gly Trp Tyr
20   25   30   35

GAT CAC AAC CCC CAT GGG   319
Asp His Asn Pro His Gly
                40

(2) INFORMATION FOR SEQ ID NO: 48:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 260 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 204..251
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.5
                                    seq LLTFLAFTTLLFA/PP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ACTGTTATTC TTCACATATT ATCTCTATTA GTADVWGGCT TCTAGTCACC CAAGTTAGAA   60

ATCTGTGAGT CATCTTTTGT TTCTTCCCTT TCCCTTACTG TTTAGTTTTA ATTGCTAAGT   120

CTTGTTAATA CTACATCAGG TATGATTTTA AAAACATTTT TGATGTTCTA CTGCCACCAC   180

CTTAGTTCTG GTACTCATTT TGC ATG TTT TGT CTT TTG ACT TTC CTT GCT TTT   233
                          Met Phe Cys Leu Leu Thr Phe Leu Ala Phe
                          -15   -10

ACA ACT CTT CTT TTC GCA CCC CCA TGG   260
Thr Thr Leu Leu Phe Ala Pro Pro Trp
 -5   1

(2) INFORMATION FOR SEQ ID NO: 49:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 365 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 126..212
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.4
                                  seq LKCLLAVLSSLFA/AI

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ACAAATGTGT TATGATTTTC CAGGCCCTTC TTCATCTGCT CTCCCTTCCT TTTGAGCATT   60

ATCCCATTTC ATGCCCCCAC ACAGATTCTA GCCATACCCC ATGACTTACA ATTTCCCCAC   120

AAAGA ATG CAC TGT GGC TCC ACT CCA GGA CTT TGC CCA TGC TGG GTC CCC   170
      Met His Cys Gly Ser Thr Pro Gly Leu Cys Pro Cys Trp Val Pro
                    -25   -20   -15

TTC CTG AAA TGC CTT CTA GCT GTT CTC TCT TCC CTG TTT GCT GCC ATT   218
Phe Leu Lys Cys Leu Leu Ala Val Leu Ser Ser Leu Phe Ala Ala Ile
             -10   -5   1

TCC GTG GAC AGA CTA TAC TTG TCT TTC TGT TCT AAT TGC TCT GAA ATA   266
Ser Val Asp Arg Leu Tyr Leu Ser Phe Cys Ser Asn Cys Ser Glu Ile
              5   10   15

TAC CTC TGG CCC CCC AGC TTT CCT GCT CCC CCA TCC CCT GTA GTC CTT   314
Tyr Leu Trp Pro Pro Ser Phe Pro Ala Pro Pro Ser Pro Val Val Leu
     20   25   30

```
CTA GTT TTC CTG TGT CCC CAT GGG ACT TCT TTA TCC TTT TTG AAG CTA        362
Leu Val Phe Leu Cys Pro His Gly Thr Ser Leu Ser Phe Leu Lys Leu
 35                  40                  45                  50

CCG                                                                    365
Pro
```

(2) INFORMATION FOR SEQ ID NO:·50:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 69 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 1..48
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 8.3
                               seq VCSALLLLGIVSS/KP

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
ATG AAT TTA GTT TGT TCA GCT CTT TTA CTT CTT GGA ATA GTA TCT TCC    48
Met Asn Leu Val Cys Ser Ala Leu Leu Leu Leu Gly Ile Val Ser Ser
    -15                 -10                 -5

AAA CCC TAT ATG AGA AAG CGG                                            69
Lys Pro Tyr Met Arg Lys Arg
  1                  5
```

(2) INFORMATION FOR SEQ ID NO: 51:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 184 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 44..148
          (C) IDENTIFICATION METHOD: Von Heijne matrix

          (D) OTHER INFORMATION: score 8.3
                                  seq AAMLIGLLAWLQT/VP

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

AAATTACAAG AAAGCTGGAC TTGCCGCTGT GGTCTCAGGA GAA ATG AGT GTT CTT   55
                                                   Met Ser Val Leu
                                                   -35

GAT GAC AGG CAA AGG GAC ATC TTA GTT GTC CAG AAG CGG CAC TCT TCC   103
Asp Asp Arg Gln Arg Asp Ile Leu Val Val Gln Lys Arg His Ser Ser
    -30   -25   -20

CTG GAA GCC GCC ATG TTA ATA GGA TTA CTA GCC TGG CTC CAG ACA GTG   151
Leu Glu Ala Ala Met Leu Ile Gly Leu Leu Ala Trp Leu Gln Thr Val
-15   -10   -5   1

CCT GCT CAT GGC TGC CAG TTC TTA CCG ATC CGG   184
Pro Ala His Gly Cys Gln Phe Leu Pro Ile Arg
            5   10

(2) INFORMATION FOR SEQ ID NO: 52:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 251 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 138..197
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 8.3
                                  seq LLIICHYLPLSLC/IP

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AATTTTTTTT CACTTTCCTA AAAGCCTTCC CTTTGCCCAT GATGCCAATG ACTAGCTCTG   60

TCCTGAAGCA ATAGCTAGTA CTTTCCCTCC TTCCTGCCAC CTAGCATCCA GCCGAACCTT   120

GAATCAATAC CAGTAAA ATG GGT GTG AAC GGA AGG AGG CTG CTC ATT ATT   170
                   Met Gly Val Asn Gly Arg Arg Leu Leu Ile Ile
                   -20   -15   -10

TGC CAT TAT TTA CCT CTG AGT CTG TGC ATT CCC ATT CCT TCC CAT ATT   218
Cys His Tyr Leu Pro Leu Ser Leu Cys Ile Pro Ile Pro Ser His Ile
              -5   1   5

AAT TCT CTC CCG CGC AAC ACC CCC CCT GTC AGG   251

Asn Ser Leu Pro Arg Asn Thr Pro Pro Val Arg
      10   15

(2) INFORMATION FOR SEQ ID NO: 53:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 154 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 26..118
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.2
                                   seq LECLLLYLAESSG/LR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACAGAACTAA CCTAGAAAGA ATGAT ATG AAA CTT CGT GAG TGC CCG GCC CTC   52
                             Met Lys Leu Arg Glu Cys Pro Ala Leu
                                 -30   -25

CGA TGG TCC CAG CTG TCC CAG CAC AAG CTG GAG TGT CTA TTG CTT TAC   100
Arg Trp Ser Gln Leu Ser Gln His Lys Leu Glu Cys Leu Leu Leu Tyr
    -20   -15   -10

CTG GCA GAG AGC TCC GGG CTC AGA ACA GGA AAT GTG GGA GTT CTC CAC   148
Leu Ala Glu Ser Ser Gly Leu Arg Thr Gly Asn Val Gly Val Leu His
    -5   1   5   10

CCA AGG   154
Pro Arg

(2) INFORMATION FOR SEQ ID NO: 54:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 485 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:

```
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 78..404
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:   score 8.2
                                 seq LLRLPQLPPXCSA/GE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:


ACCCTTTCGT CCGCTCTCAT TGGCTCTGCT GCAGCCCTGA CCAACGCTCC AATAGGCCGG    60

GATCCAGCCA TACTTCA ATG GAT CCC AGG GGT ATC TTG AAG GCA TTT CCC       110
                    Met Asp Pro Arg Gly Ile Leu Lys Ala Phe Pro
                                 -105                -100

AAG CGG CAG AAA ATT CAT GCT GAT GCA TCA TCA AAA GTA CTT GCA AAG      158
Lys Arg Gln Lys Ile His Ala Asp Ala Ser Ser Lys Val Leu Ala Lys
            -95             -90                 -85

ATT CCT AGG AGG GAA GAG GGA GAA GAA GCA GAA GAG TGG CTG AGC TCC      206
Ile Pro Arg Arg Glu Glu Gly Glu Glu Ala Glu Glu Trp Leu Ser Ser
            -80             -75                 -70

CTT CGG GCC CAT GTT GTG CGC ACT GGC ATT GGA CGA GCC CGG GCA GAA      254
Leu Arg Ala His Val Val Arg Thr Gly Ile Gly Arg Ala Arg Ala Glu
    -65                 -60             -55

CTC TTT GAG AAG CAG ATT GTT CAG CAT GGC GGC CAG CTA TGC CCT GCC      302
Leu Phe Glu Lys Gln Ile Val Gln His Gly Gly Gln Leu Cys Pro Ala
-50             -45                 -40                 -35

CAG GGC CCA GGT GTC ACT CAC ATT GTG GTG GAT GAA GGC ATG GAC TAT      350
Gln Gly Pro Gly Val Thr His Ile Val Val Asp Glu Gly Met Asp Tyr
                -30             -25                 -20

GAG CGA GCC CTC CGC CTT CTC AGA CTA CCC CAG CTG CCC CCG GKT TGC      398
Glu Arg Ala Leu Arg Leu Leu Arg Leu Pro Gln Leu Pro Pro Xaa Cys
            -15             -10                 -5

TCA GCT GGT GAA GTC AGC CTG GCT GAG CTT GTG CCT TCA GGA GAG GAG      446
Ser Ala Gly Glu Val Ser Leu Ala Glu Leu Val Pro Ser Gly Glu Glu
            1               5                   10

GCT GGT GGA TGT AGC TGG ATT CAG CAT CTT CAT CCC AGT                  485
Ala Gly Gly Cys Ser Trp Ile Gln His Leu His Pro Ser
15               20                  25
```

(2) INFORMATION FOR SEQ ID NO: 55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 276 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 199..261
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 8
                              seq LFLVAVLVKVAEA/RK

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

AGCCTCTCCT GCACCCTCAG CCGGCGCGCT TCTCTTATGG GCGTCTGCTG CAGTCTGGCT   60

GCGGTCGAAC TGAAAGCGGC GGCGGGAGAC CAAACTTAGA CCCCGCTGTG GACTAGAGAA   120

CTCAGAGAAG GCAGAGGGAG AGGGAGAGAG AGASABWBAA GGGACCCGAG GAGGAGGCTT   180

CCATCACGTC ATTGCAGG ATG TTC TGG AAG CTT TCC CTG TCC TTG TTC CTG   231
                    Met Phe Trp Lys Leu Ser Leu Ser Leu Phe Leu
                        -20   -15

GTG GCG GTG CTG GTG AAG GTG GCG GAA GCC CGG AAG AAC CGG TCG   276
Val Ala Val Leu Val Lys Val Ala Glu Ala Arg Lys Asn Arg Ser
-10   -5   1   5

(2) INFORMATION FOR SEQ ID NO: 56:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 197 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 120..173
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 7.9
                              seq LFSLLVLQSMATG/AT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AAGTTTCCCG GGAGAGACGA AAGCAGGAAC GAGAGCGGAG GNAGCACAGT CCGCCGAGCA   60

CAAGCTCCAG CATCCCGTCA GGGGTTGCAG GTGTGTGGGA GGCTTGAAAC TGTTACAAT   113

ATG GCT TTC CTT GGA CTC TTC TCT TTG CTG GTT CTG CAA AGT ATG GCT   167
Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala
        -15   -10   -5

ACA GGG GCC ACT TTC CCT GAG GAA GCC CCG   197

Thr Gly Ala Thr Phe Pro Glu Glu Ala Pro
    1   5

(2) INFORMATION FOR SEQ ID NO: 57:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 299 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 90..143
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.9
                                    seq LFSLLVLQSMATG/AT

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

AGAGAGCGGA SSTAGCACAG TCCGCCGAGC ACAAGCTCCA GCATCCCGTC AGGGTTGCAG   60

GTGTGTGGGA GGCTTGAAAC TGTTACAAT ATG GCT TTC CTT GGA CTC TTC TCT   113
                                 Met Ala Phe Leu Gly Leu Phe Ser
                                                  -15

TTG CTG GTT CTG CAA AGT ATG GCT ACA GGG GCC ACT TTC CCT GAG GAA   161
Leu Leu Val Leu Gln Ser Met Ala Thr Gly Ala Thr Phe Pro Glu Glu
-10   -5   1   5

GCC ATT GCT GAC TTG TCA GTG AAT ATG TAT AAT CGT CTT AGA GCA GTT   209
Ala Ile Ala Asp Leu Ser Val Asn Met Tyr Asn Arg Leu Arg Ala Val
                10   15   20

GGA AGC TGG AGA AGG GAA GGA GCC AGC AGA CAA ATT GCT TCG TGT CTG   257
Gly Ser Trp Arg Arg Glu Gly Ala Ser Arg Gln Ile Ala Ser Cys Leu
            25   30   35

CCT GCC TTT CTC CTC CAT TTA CCC CTT ACA CAC ACA CAC GGG   299
Pro Ala Phe Leu Leu His Leu Pro Leu Thr His Thr His Gly
    40   45   50

(2) INFORMATION FOR SEQ ID NO: 58:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 370 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 62..226
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 7.8
                        seq ALLVALLFTLIHR/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:


```
AAGTGAGAAA GGAGCTTACC AAAGGCAGTG TACGAAGAAG GTTCCTGGGA GACTGTCAGA   60

A ATG AGT TTT TCA CTG AAC TTC ACC CTG CCG GCG AAC ACA ACG TCC TCT   109
  Met Ser Phe Ser Leu Asn Phe Thr Leu Pro Ala Asn Thr Thr Ser Ser
  -55              -50                 -45                 -40

CCT GTC ACA GGT GGG AAA GAA ACG GAC TGT GGG CCC TCT CTT GGA TTA    157
Pro Val Thr Gly Gly Lys Glu Thr Asp Cys Gly Pro Ser Leu Gly Leu
            -35                 -30                 -25

GCG GCG GGC ATA CCA TTG CTG GTG GCC ACA GCC CTG CTG GTG GCT TTA    205
Ala Ala Gly Ile Pro Leu Leu Val Ala Thr Ala Leu Leu Val Ala Leu
            -20                 -15                 -10

CTA TTT ACT TTG ATT CAC CGA AGA AGA AGC AGC ATT GAG GCC ATG GAG    253
Leu Phe Thr Leu Ile His Arg Arg Arg Ser Ser Ile Glu Ala Met Glu
        -5              1               5

GAA AGT GAC AGA CCA TGT GAA ATT TCA GAA ATT GAT GAC AAT CCC AAG    301
Glu Ser Asp Arg Pro Cys Glu Ile Ser Glu Ile Asp Asp Asn Pro Lys
 10              15              20                  25

ATA TCT GAG AAT CCT AGG AGA TCA CCC ACA CAT GAG AAG AAT ACG ATG    349
Ile Ser Glu Asn Pro Arg Arg Ser Pro Thr His Glu Lys Asn Thr Met
                30              35                  40

GGA GCA CAA GAG GCC CGC TGG                                        370
Gly Ala Gln Glu Ala Arg Trp
            45
```


(2) INFORMATION FOR SEQ ID NO: 59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 336 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 91..330
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 7.7
                                     seq LVLFLSLALLVTP/TS


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:


TATTCCTTGG AGTTCCACGA CTGAATTAAG ACTGTTGTGG GRDCCATAAT TTTCAAATAC      60

TTGCCCTATA TTCGTGTTGA GGGTTCACAC ATG AGC ACA TGG TAT TTG GCA CTT      114
                                 Met Ser Thr Trp Tyr Leu Ala Leu
                                 -80                 -75

AAT AAG TCC TAT AAG AAT AAA GAC AGC GTT AGG ATT TAT CTC AGC TTG      162
Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu
        -70             -65             -60

TGC ACA GTG AGC ATT AAA TTT ACA TAC TTT CAT GAT ATA CAG ACT AAT      210
Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn
    -55             -50             -45

TGT CTT ACA ACA TGG AAA CAT TCG AGA TGC AGA TTT TAT TGG GCA TTT      258
Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe
-40             -35             -30             -25

GGT GGT TCC ATT TTA CAG CAC TCA GTG GAT CCC CTT GTT TTG TTC CTA      306
Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu
            -20             -15             -10

AGC CTG GCC CTG TTA GTG ACA CCC ACT TCG                              336
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser
        -5                   1



(2) INFORMATION FOR SEQ ID NO: 60:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 394 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 266..322
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 7.7
                                    seq LQLLCCIFTLVLQ/HY

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:
```

```
ATACTATAAG GCTAGAATTG ACTTGGAGTC AAGGCGAGTT CCATAGGTTT AATGCGTGGC     60

ACCTATCTCA ACAACTGCAA AATCACTGTA ACTTGTAAAA AATCCCAGGG CCACTCATGG    120

ACAGCCACAT CTTTAAACCC ACACAAAAAT ACAGACACTT TGATTACATG AAAGTTAGAA    180

GCTCTAAACT AGAGCAAGGT CAGTTGTGGT AAGAAGGTAT TAGATTCAAG CATCCACAAA    240

AGTTTATAGT CTGTCAGTCA TAAGG ATG GCT ATT GGG ATT TCT TTA CAG TTA     292
                            Met Ala Ile Gly Ile Ser Leu Gln Leu
                                                       -15

CTC TGT TGT ATT TTC ACT TTG GTT TTA CAG CAC TAT CTC TTA GGA AGT    340
Leu Cys Cys Ile Phe Thr Leu Val Leu Gln His Tyr Leu Leu Gly Ser
-10              -5                  1               5

CAT CCA TAT ATT ACC TGC ATA CAC AGT CAG CTT CTT CTC GAT ATA CAG    388
His Pro Tyr Ile Thr Cys Ile His Ser Gln Leu Leu Leu Asp Ile Gln
            10              15                  20

CAG CAG                                                             394
Gln Gln
```

```
(2) INFORMATION FOR SEQ ID NO: 61:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 429 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 208..264
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 7.6
                                    seq LLNLLLLSLFAGL/DP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:
```

```
GAGAATGCCT GCNGAATGAT CGCCCCCCAG GGCGGCTGCC GCCGCTGCCG CTGCTGCTGT     60

TATTGCTACT GCTGCTGCCG CCGCCTCTGC TTCCACTCGG CTCTGACTGG CAGGCARAAA    120

RTGCAACTTG AMSGARGGRH ARGTCTCTGG CAGTGAGTGG AGAGCCTACA TAAAAGAGAG    180

TAAAGAGGGG CAAAAACCCA GATCAGA ATG CAG GCG ACG TCC AAC CTT CTC AAC    234
                              Met Gln Ala Thr Ser Asn Leu Leu Asn
                                                             -15
```

```
CTC CTG CTG CTG TCT TTG TTT GCC GGA TTA GAT CCT TCC AAG AAC AAA    282
Leu Leu Leu Leu Ser Leu Phe Ala Gly Leu Asp Pro Ser Lys Asn Lys
-10              -5                  1                   5

AAG AGA GGA AGT TCT TTT TCA TTT AAG TTT CCT TTA CTA GAT GAT ACC    330
Lys Arg Gly Ser Ser Phe Ser Phe Lys Phe Pro Leu Leu Asp Asp Thr
            10              15                  20

CCA TTC CTA NGA TCC AGA ATT GAA AAT AGT GCT ACA CAT CAT CTA CAC    378
Pro Phe Leu Xaa Ser Arg Ile Glu Asn Ser Ala Thr His His Leu His
        25              30                  35

TAT GGA CTA AAC ATG ATT CTG TGG GTT AAT TGG AAA CCT AAG CTC ACT    426
Tyr Gly Leu Asn Met Ile Leu Trp Val Asn Trp Lys Pro Lys Leu Thr
    40              45                  50

TTG                                                                429
Leu
55
```

(2) INFORMATION FOR SEQ ID NO: 62:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 189 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 88..180
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.6
                                     seq VTLLCGWPGSHWC/AP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```
AACAGGCGTA ASKACATGGC CCAGCTCGAT CCCTCCCTTT TGTTCAACAA ACTAAATTCG    60

AGCAGGAGGC TCTAGGATTC CACAGGC ATG ATG AAA TGG AAG CCG GAG GAT CTG   114
                            Met Met Lys Trp Lys Pro Glu Asp Leu
                                -30                 -25

GGA TCG GTT CCT TGT GAG GCT TTC TCT GTT ACT CTG CTG TGC GGC TGG    162
Gly Ser Val Pro Cys Glu Ala Phe Ser Val Thr Leu Leu Cys Gly Trp
        -20             -15                 -10

CCA GGG TCG CAT TGG TGT GCC CCA CCA                                189
Pro Gly Ser His Trp Cys Ala Pro Pro
    -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 63:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 243 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 10..66
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7.6
                              seq LLNLLLLSLFAGL/DP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:


```
AAGATCAGA ATG CAG GCG ACG TCC AAC CTT CTC AAC CTC CTG CTG CTG TCT      51
          Met Gln Ala Thr Ser Asn Leu Leu Asn Leu Leu Leu Leu Ser
                   -15                     -10

TTG TTT GCC GGA TTA GAT CCT TCC AAG ACT CAG ATT AGT CCT AAA GAA       99
Leu Phe Ala Gly Leu Asp Pro Ser Lys Thr Gln Ile Ser Pro Lys Glu
 -5              1           5               10

GGG TGG CAG GTG TAC AGC TCA GCT CAG GAT CCT GAT GGG CGG TGC ATT      147
Gly Trp Gln Val Tyr Ser Ser Ala Gln Asp Pro Asp Gly Arg Cys Ile
        15              20              25

TGC ACA GTT GTW GCT CCA GAA CAA AAC CTG TGT TCC CGG GAT GCC AAA      195
Cys Thr Val Val Ala Pro Glu Gln Asn Leu Cys Ser Arg Asp Ala Lys
        30              35              40

AGC AGG CAA CTT CGC CAA CTA CTG GAA AAG GTT CAG AAC ATG TCC CGG      243
Ser Arg Gln Leu Arg Gln Leu Leu Glu Lys Val Gln Asn Met Ser Arg
    45              50              55
```


(2) INFORMATION FOR SEQ ID NO: 64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 397 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 158..301
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION:  score 7.5
                                        seq FVILLLFIFTVVS/LV


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:
```

ACAAACAGAC GMTACCATCG CTTCAGCAGC ATCCTCTCAG ACAAGAGCCA CTATTTCTGA   60

TTCAGATCAC CTGTCATCGA AGTTTAAAGA AGGGGAAACA GGAGACAGAA ATACACTGAA   120

CCAAAAAGAT TCAAAGAGC AAGTGGAATC TCTAAGA ATG GCT TCC AGC CAC TGG   175
                                         Met Ala Ser Ser His Trp
                                                          -45

AAT GAA ACC ACT ACC TCT GTT TAT CAG TAC CTT GGT TTT CAA GTT CAA   223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
        -40   -35   -30

AAA ATT TAC CCT TTC CAT GAC AAC TGG AAC ACT GCC TGC TTT GTC ATC   271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
    -25   -20   -15

CTG CTT TTA TTT ATA TTT ACA GTG GTA TCT TTA GTG GTG CTG GCT TTC   319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
-10   -5   1   5

CTT TAT GAA GTG CTT GAC TGC TGC TGC TGT GTA AAA AAC AAA ACC GTG   367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val
            10   15   20

AAA GAC TTG AAA AGT GAA CCC AAC CCT CGG   397
Lys Asp Leu Lys Ser Glu Pro Asn Pro Arg
        25   30

(2) INFORMATION FOR SEQ ID NO: 65:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 182 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 78..176
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 7.4
                                        seq ITCCVLLLLNCSG/VW
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:


ATCGACTGTG AGCTGCGGCA GAGAGCAGAG GCGGCGGCGC GGGACCTGCA GTCGCCAGGG     60

ATTCCCTCCA GGTGACG ATG CTC TGG TTC TCC GGC GTC GGG GCT CTG GCT        110
                   Met Leu Trp Phe Ser Gly Val Gly Ala Leu Ala
                        -30                       -25

GAG CGT TAC TGC CGC CGC TCG CCT GGG ATT ACG TGC TGC GTC TTG CTG       158
Glu Arg Tyr Cys Arg Arg Ser Pro Gly Ile Thr Cys Cys Val Leu Leu
     -20               -15               -10

CTA CTC AAT TGC TCA GGG GTC TGG                                       182
Leu Leu Asn Cys Ser Gly Val Trp
     -5                1




(2) INFORMATION FOR SEQ ID NO: 66:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 256 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 164..238
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.3
                                  seq LIFFLNVTQLVRG/RG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:


AGTAAATAAA AAGTTTGCTT TATTAAATTA TGTTTAGATA GTGSTTATAG TGCTTTACCC      60

CTTCAAAATA GTAACTTCTA TCAATCATTT AGGATGTGTG TCAGACTATT CTGTGTCCTT     120

TAAGTGTGTK AACTAGTTTT AACCCTCTGC AAATATCTGA GGT ATG CTC TTT TTA      175
                                               Met Leu Phe Leu
                                                    -25

CAG ATG GGA AAA CAA TCT TGG ACT TTA ATA TTT TTT CTT AAT GTT ACA      223
Gln Met Gly Lys Gln Ser Trp Thr Leu Ile Phe Phe Leu Asn Val Thr
     -20               -15               -10

CAA TTA GTA AGA GGC AGG GGG CCA GGC GGA CGG                          256
Gln Leu Val Arg Gly Arg Gly Pro Gly Gly Arg
     -5                1                 5

(2) INFORMATION FOR SEQ ID NO: 67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 19..99
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 7.2
                            seq LLLGLCSPPXXSL/AS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:


AATTGATTAG GAGATTAT ATG GAG CTG CGG GAS NTG CCG CCT GGG GGA AGA          51
                  Met Glu Leu Arg Xaa Xaa Pro Pro Gly Gly Arg
                      -25              -20

GAG GTG CAG CTT CTG CTA GGT TTG TGC TCT CCT CCC AGS RTC TCC TTG          99
Glu Val Gln Leu Leu Leu Gly Leu Cys Ser Pro Pro Xaa Xaa Ser Leu
   -15              -10              -5

GCT TCC TTC CCC AAA GCA GCT CAG ATG                                     126
Ala Ser Phe Pro Lys Ala Ala Gln Met
 1              5



(2) INFORMATION FOR SEQ ID NO: 68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 117 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 46..87
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 7
                            seq LWSLLSSSGSHFG/IP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```
AGCAGGCCTT TGGGAGAGAA ACCTAATGCC TAAGCCTCAT CCTTT ATG CTC TGG TCT    57
                                                   Met Leu Trp Ser
```

```
CTT CTT TCC TCT TCA GGC TCA CAT TTT GGT ATC CCT CAC CAC ACA TTT    105
Leu Leu Ser Ser Ser Gly Ser His Phe Gly Ile Pro His His Thr Phe
-10               -5              1               5
```

```
CCC CAA GAA GGG                                                     117
Pro Gln Glu Gly
          10
```

(2) INFORMATION FOR SEQ ID NO: 69:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 445 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 110..265
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7
                                   seq SVWLCLLCYFAFP/FQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```
ATGCACCATG ATATTTTTAT ACACGTTGTG TTAACTACTG TAAACACATT GTCTTCTTTA    60
```

```
TATTTCTTTG CAGGAAGTTC AGAAAAAAGT GTCACGTTTT AATCTGCAG ATG GAC ATA   118
                                                      Met Asp Ile
                                                          -50
```

```
AGT GGA TTA ATT CCT GGT CTA GTG TCT ACA TTC ATA CTT TTG TCT AKH    166
Ser Gly Leu Ile Pro Gly Leu Val Ser Thr Phe Ile Leu Leu Ser Xaa
              -45             -40             -35
```

```
AGT GAT CAC TAC GGA CGA AAA TTC CCT ATG ATT TTG TCT TCC GTT GGT    214
Ser Asp His Tyr Gly Arg Lys Phe Pro Met Ile Leu Ser Ser Val Gly
          -30             -25             -20
```

```
GCT CTT GCA ACC AGC GTT TGG CTC TGT TTG CTT TGC TAT TTT GCC TTT    262
Ala Leu Ala Thr Ser Val Trp Leu Cys Leu Leu Cys Tyr Phe Ala Phe
      -15             -10             -5
```

```
CCA TTC CAG CTT TTG ATT GCA TCT ACC TTC ATT GGT GCA TTT NGT GGC    310
Pro Phe Gln Leu Leu Ile Ala Ser Thr Phe Ile Gly Ala Phe Xaa Gly
    1               5               10              15
```

```
AAT TAT ACC ACA TTT TGG GGA GCT TGC TTT GCC TAT ATA GTT GAT CAG    358
```

```
Asn Tyr Thr Thr Phe Trp Gly Ala Cys Phe Ala Tyr Ile Val Asp Gln
            20              25              Tyr         30
```

```
TGT AAA GAA CRS DKA CAA AAA ACA ATT CGA ATA GCT ATC ATT GAC TTT      406
Cys Lys Glu Xaa Xaa Gln Lys Thr Ile Arg Ile Ala Ile Ile Asp Phe
            35              40              Ile         45
```

```
CTA CTT GGA CTT GTT ACT GGA CTA ACA GTA CTG TCA TCT                  445
Leu Leu Gly Leu Val Thr Gly Leu Thr Val Leu Ser Ser
            50              55              60
```

(2) INFORMATION FOR SEQ ID NO: 70:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 137..226
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7
                                seq LFVILLITSLIFC/SL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```
ACTTTTTGAA TTTGTTGCTG GTACAGTTGC ATGTATTCTC TTAAAATTAT TTTGAGGCCT      60

CATATCTGGT TATTTCTCCT TTCTCATTCC TTATCTTGCG TGTTTTTACC TTTTTTTCAT     120

AACTAAGTTT TTGAGG ATG TWA GTG TTC TTT TCA AAG AAC CGG TTC GAA ATG     172
               Met Xaa Val Phe Phe Ser Lys Asn Arg Phe Glu Met
               -30              -25              -20
```

```
TAC TTT TCT TTG CTA CTT TTT GTT ATT TTA TTG ATC ACA TCT TTA ATC      220
Tyr Phe Ser Leu Leu Leu Phe Val Ile Leu Leu Ile Thr Ser Leu Ile
            -15              -10              -5
```

```
TTT TGT TCT CTA TAC GTG GCG CGT                                      244
Phe Cys Ser Leu Tyr Val Ala Arg
            1               5
```

(2) INFORMATION FOR SEQ ID NO: 71:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 390 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE

```
                    (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                    (A) ORGANISM: Homo Sapiens
                    (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                    (A) NAME/KEY: sig_peptide
                    (B) LOCATION: 289..357
                    (C) IDENTIFICATION METHOD: Von Heijne matrix
                    (D) OTHER INFORMATION:  score 6.9
                                      seq SLSLLASHHSVSC/SN

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:
```

```
AAGTACAAAG CCTACTCCAA AGACTGCAGC TTGAAGATAA AAGAGAGCAC TGCGTCCTTT     60

TGAAAATAAA GGCAGACACA AAGAAGAAAG GAGCTACCTT ACCCCAGCAT ATACCTGCGG    120

GATGTTCTCT CCAGTTCATT TTTACCTGGT GTCTTGAAAT CCGAGCAATT CCTAAAAAGG    180

CATTTTTGCG AGCCCTTGTG GACTATACCA GTGACAGTGC TGAAAAGCGC AGGCTACAGG    240

AGCTGTGCAG TAAACAAGGG GCAGCCGATT ATAGCCGCTT TGTACGAG ATG CCT GTG    297
                                                     Met Pro Val

CCT GCT TGT TGG ATC TCC TCC TCG CTT TCC CTT CTT GCC AGC CAC CAC    345
Pro Ala Cys Trp Ile Ser Ser Ser Leu Ser Leu Leu Ala Ser His His
-20                -15                -10                     -5

TCA GTC TCC TGC TCG AAC ATC TTC CTA AAC TTC AAC CCA GAC CGG        390
Ser Val Ser Cys Ser Asn Ile Phe Leu Asn Phe Asn Pro Asp Arg
                  1                5                   10
```

```
(2) INFORMATION FOR SEQ ID NO: 72:

        (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 374 base pairs
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: DOUBLE
                    (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                    (A) ORGANISM: Homo Sapiens
                    (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                    (A) NAME/KEY: sig_peptide
                    (B) LOCATION: 198..260
                    (C) IDENTIFICATION METHOD: Von Heijne matrix
                    (D) OTHER INFORMATION:  score 6.9
                                      seq LLACGSLLPGLWQ/HL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:
```

```
ATATATTTCT GAGGCAGTAC CCATCTCACT TGTAAACTTA AAAGACACCG CAGAGATTTG      60

AGGGACTCAG AAGTCAAATA GAGTAGGTTA AAAACCTCTT ATTTTTCAAA TTAATTGTTT     120

TAAGAAACAA GCATACCTGT GTAAGTGAAA TATCTTAATT TGTGTTGAAT CAAGTTAGGA     180

GACAGAGATT CTCATGA ATG TGT CCT GTG TTC TCA AAG CAG CTG CTA GCC       230
                   Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
                   -20                    -15

TGT GGG TCT CTC CTA CCT GGG TTA TGG CAG CAC CTC ACA GCC AAT CAC     278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His
-10                  -5                  1                   5

TGG CCT CCA TTC TCC SCT TTC CTC TGT ACA GTT TGC TCT GGT TCC TCA     326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
                 10                  15                  20

GAG CAG ATT TCC GAG TAT ACT GCT TCA GCC ACG CCC CCA CTG TGC CTG     374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Leu
        25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 73:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 416 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 33..260
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.9
                        seq LLPLSAWPPWAWH/HH

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```
ACGCTCAGCA GGTCCACTCC CGTGTTCCGG TC ATG GCT TTA ACA ATT CAT GGG       53
                                  Met Ala Leu Thr Ile His Gly
                                  -75                   -70

GAA AGA ATG CGC CCC GAT TGG GAG AGC CCC TGG ATC ACG TCT TCC CAA      101
Glu Arg Met Arg Pro Asp Trp Glu Ser Pro Trp Ile Thr Ser Ser Gln
            -65                  -60                  -55

GCT CAG TCC CTC TCT CTT GGA GGG AGT CCG TCC TCG AGG GGC CCT CTG      149
Ala Gln Ser Leu Ser Leu Gly Gly Ser Pro Ser Ser Arg Gly Pro Leu
        -50                  -45                  -40
```

```
GTG CCC AGG GGA GAG TAT CTT GCG TCC TGT CCT GAG GGC GTC CGC TCA        197
Val Pro Arg Gly Glu Tyr Leu Ala Ser Cys Pro Glu Gly Val Arg Ser
        -35             -30             -25

CAC AGC CAC CTG CTC CCC CGC TCC CTC CTT CCC TTG TCA GCA TGG CCA        245
His Ser His Leu Leu Pro Arg Ser Leu Leu Pro Leu Ser Ala Trp Pro
        -20             -15             -10

CCG TGG GCC TGG CAT CAC CAT GGG CCT GGC ACA CAG TCC CTC GTG GGC        293
Pro Trp Ala Trp His His His Gly Pro Gly Thr Gln Ser Leu Val Gly
    -5               1               5               10

TGC CTT TGT GCC ATG AGC CCA CTG CTG CCG ACT CAC CTG TCC CTC CCA        341
Cys Leu Cys Ala Met Ser Pro Leu Leu Pro Thr His Leu Ser Leu Pro
            15              20              25

GTA CTG GAA CCT TCT GGA ACA CCA GCA CTA AAA GAT AGG AGG CCC TGT        389
Val Leu Glu Pro Ser Gly Thr Pro Ala Leu Lys Asp Arg Arg Pro Cys
        30              35              40

GAG GTT GGC ATC CCC ATC CCC CCC AGG                                     416
Glu Val Gly Ile Pro Ile Pro Pro Arg
    45              50
```

(2) INFORMATION FOR SEQ ID NO: 74:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 295 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 11..286
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.8
                             seq ILIASSLPTLSHP/AP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```
AAGAGTCACA ATG GCA GCC AGA TTC AGG TGC GGC CAT TTG TGT GTC CCC         49
           Met Ala Ala Arg Phe Arg Cys Gly His Leu Cys Val Pro
               -90             -85             -80

GAG GTT CCT CGC GGG CCG GCA TCC CAC GCC GAG GGT GGT GGT GGC AGG        97
Glu Val Pro Arg Gly Pro Ala Ser His Ala Glu Gly Gly Gly Gly Arg
        -75             -70             -65

CTT TCC AGA AAG GCA GCA CAC CAG GCT CAG CTC TGC TGG CGA GCA GGA       145
Leu Ser Arg Lys Ala Ala His Gln Ala Gln Leu Cys Trp Arg Ala Gly
```

```
      -60                           -55                        -50
GGC GAC GGC AGA GGA AAC TTC AAC CCG ATG AAC TTC CTG GTT GCG GGG     193
Gly Asp Gly Arg Gly Asn Phe Asn Pro Met Asn Phe Leu Val Ala Gly
          -45                   -40                   -35

ACA TTT GCC TCC TCC TGC CAC TCA CCA CCT CTG CTC TGG TCC CTC CCT     241
Thr Phe Ala Ser Ser Cys His Ser Pro Pro Leu Leu Trp Ser Leu Pro
      -30                   -25                   -20

CCA AGA ATC CTC ATA GCG TCC TCT CTC CCC ACT CTC TCC CAT CCC GCG     289
Pro Arg Ile Leu Ile Ala Ser Ser Leu Pro Thr Leu Ser His Pro Ala
-15                   -10                   -5                    1

CCT GGG                                                             295
Pro Gly
```

(2) INFORMATION FOR SEQ ID NO: 75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 361 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 101..187
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.8
                                seq VLSLICSCFYTQP/HP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```
ACTCTCCCCT CCCCTCCCCG GCACTGCAGC ACCAGCCGTC TGCAGCTCCG GCCGCCACTT     60

GCGCCTCTCC AGCCTCCGCA GCCCAACCGC CGCCAGCACC ATG GCC AGC ACC ATT     115
                                            Met Ala Ser Thr Ile
                                                              -25

TCC GCC TAC AAG GAG AAG ATG AAG GAG CTG TCG GTG CTG TCG CTC ATC     163
Ser Ala Tyr Lys Glu Lys Met Lys Glu Leu Ser Val Leu Ser Leu Ile
              -20                   -15                   -10

TGC TCC TGC TTC TAC ACA CAG CCG CAC CCC AAT ACC GTC TAC CAG TAC     211
Cys Ser Cys Phe Tyr Thr Gln Pro His Pro Asn Thr Val Tyr Gln Tyr
          -5                    1                     5

GGG GAC ATG GAG GTG AAG CAG CTG GAC AAG CGG GCC TCA GGC CAG AGC     259
Gly Asp Met Glu Val Lys Gln Leu Asp Lys Arg Ala Ser Gly Gln Ser
    10                    15                    20
```

```
TTC GAG GTC ATC CTC AAG TCC CCT TCT GAC CTG TCC CCA GAG AGC CCT    307
Phe Glu Val Ile Leu Lys Ser Pro Ser Asp Leu Ser Pro Glu Ser Pro
 25                  30                  35                  40

ATG CTC TCC TCC CCA CCC AAG AAG AAG GAC ACC TCC CTG GAG GAG CTG    355
Met Leu Ser Ser Pro Pro Lys Lys Lys Asp Thr Ser Leu Glu Glu Leu
                45                  50                  55

CAA AAG                                                             361
Gln Lys
```

(2) INFORMATION FOR SEQ ID NO: 76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 361 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 2..343
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.7
                             seq LIPMAILLGQTQS/NS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
A ATG TTA CAA GTC TAT GGA AAG CCA GTT TAT CAG GGC CAT CGA AGC ACT    49
  Met Leu Gln Val Tyr Gly Lys Pro Val Tyr Gln Gly His Arg Ser Thr
            -110                -105                -100

CTT AAA AAA GGA CCA TAT CTC AGA TTT AAT TCT CCA TCT CCT AAG TCC       97
Leu Lys Lys Gly Pro Tyr Leu Arg Phe Asn Ser Pro Ser Pro Lys Ser
            -95                 -90                 -85

AGA CCA CAG AGA CCA AAA GTA ATA GAA CGA GTT AAA GGC ACT AAG GTA      145
Arg Pro Gln Arg Pro Lys Val Ile Glu Arg Val Lys Gly Thr Lys Val
        -80                 -75                 -70

AAG TCA ATA AGA ACA CAG ACT GAC TTC TAT GCA ACA AAA CCT AAG AAG      193
Lys Ser Ile Arg Thr Gln Thr Asp Phe Tyr Ala Thr Lys Pro Lys Lys
        -65                 -60                 -55

ATG GAT TCT AAA ATG AAA CAT TCT GTT CCT GTG TTA CCT CAT GGC GAT      241
Met Asp Ser Lys Met Lys His Ser Val Pro Val Leu Pro His Gly Asp
-50                 -45                 -40                 -35

CAG CAA TAT TTG TTC AGC CCA AGT AGA GAA ATG CCT ACT TTT TCA GGT      289
Gln Gln Tyr Leu Phe Ser Pro Ser Arg Glu Met Pro Thr Phe Ser Gly
            -30                 -25                 -20
```

```
ACA TTG GAA GGT CAT CTG ATT CCT ATG GCA ATT CTT TTA GGA CAA ACC      337
Thr Leu Glu Gly His Leu Ile Pro Met Ala Ile Leu Leu Gly Gln Thr
        -15                 -10                 -5


CAA AGT AAT AGT GAT ACC ATG CCG                                      361
Gln Ser Asn Ser Asp Thr Met Pro
        1               5
```

(2) INFORMATION FOR SEQ ID NO: 77:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 388 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 8..361
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 6.7
                              seq LLFAKLFGHLTSA/RR

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```
AGCAGAC ATG TCT GTA CTT GAA ATC AGT GGA ATG ATA ATG AAC AGA GTG      49
        Met Ser Val Leu Glu Ile Ser Gly Met Ile Met Asn Arg Val
            -115                -110                -105

AAC AGC CAT ATA CCA GGA ATA GGA TAC CAG ATT TTT GGA AAT GCA GTC      97
Asn Ser His Ile Pro Gly Ile Gly Tyr Gln Ile Phe Gly Asn Ala Val
            -100                -95                 -90

TCT CTC ATA CTG GGT TTA ACT CCA TTT GTT TTC CGA CTT TCT CAA GCT     145
Ser Leu Ile Leu Gly Leu Thr Pro Phe Val Phe Arg Leu Ser Gln Ala
            -85                 -80                 -75

ACA GAC TTG GAA CAA CTC ACA GCA CAT TCT GCT TCA GAA CTT TAT GTG     193
Thr Asp Leu Glu Gln Leu Thr Ala His Ser Ala Ser Glu Leu Tyr Val
            -70                 -65                 -60

ATT GCA TTT GGT TCT AAT GAA GAT GTC ATA GTT CTT TCT ATG GTT ATA     241
Ile Ala Phe Gly Ser Asn Glu Asp Val Ile Val Leu Ser Met Val Ile
        -55                 -50                 -45

ATA AGT TTT GTG GTT CGC GTG TCT CTT GTG TGG ATT TTC TTT TTT TTG     289
Ile Ser Phe Val Val Arg Val Ser Leu Val Trp Ile Phe Phe Phe Leu
    -40                 -35                 -30                 -25

CTC TGT TTA GCA GAA AGA ACT TAT AAA CAG CGA TTA CTT TTT GCA AAA     337
Leu Cys Val Ala Glu Arg Thr Tyr Lys Gln Arg Leu Leu Phe Ala Lys
            -20                 -15                 -10
```

```
CTC TTT GGA CAT TTA ACA TCT GCA AGG AGG GCT CGA AAA TCT GAG GTT    385
Leu Phe Gly His Leu Thr Ser Ala Arg Arg Ala Arg Lys Ser Glu Val
            -5                       1               5

CCT                                                                388
Pro
```

(2) INFORMATION FOR SEQ ID NO: 78:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 291 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 79..285
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 6.7
                              seq FFKLLLLGAMCSG/AR

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:


```
AAGACTTTGA CTGGAAGAGG AGAAAGAACT GCATGCTTGT AACGGCCCGG ATGGGAGTGT    60

ATTCCTTTTT TTGAAGAT ATG TGT AAA GGC ATT AAA GCT GGT GAC ACC TGT    111
                    Met Cys Lys Gly Ile Lys Ala Gly Asp Thr Cys
                                -65                     -60

GAG AAG CTG GTG GGA TAT TCT GCC GTG TAT AGA GTC TGT TTT GGA ATG    159
Glu Lys Leu Val Gly Tyr Ser Ala Val Tyr Arg Val Cys Phe Gly Met
            -55             -50             -45

GCT TGT TTC TTC TTT ATC TTC TGT CTA CTG ACC TTG AAA ATC AAC AAC    207
Ala Cys Phe Phe Phe Ile Phe Cys Leu Leu Thr Leu Lys Ile Asn Asn
        -40             -35             -30

AGC AAA AGT TGT AGA GCT CAT ATT CAC AAT GGC TTT TGG TTC TTT AAA    255
Ser Lys Ser Cys Arg Ala His Ile His Asn Gly Phe Trp Phe Phe Lys
    -25             -20             -15

CTT CTG CTG TTG GGG GCC ATG TGC TCA GGA GCA AGG                    291
Leu Leu Leu Leu Gly Ala Met Cys Ser Gly Ala Arg
-10             -5               1
```

(2) INFORMATION FOR SEQ ID NO: 79:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 402 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 61..372
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.6
                                    seq HFSHVVWFHPTWA/QQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

ATTTTCCCGG GTCTTCTCCA GCTGCCACCG CTTTACTGCA AAACTGACGG GCGCAAAAAC   60

ATG AGT GAC TCC GCG GGA GGG CGC GCT GGT CTC CGG CGT TAC CCC AAG   108
Met Ser Asp Ser Ala Gly Gly Arg Ala Gly Leu Arg Arg Tyr Pro Lys
            -100   -95   -90

CTC CCA GTG TGG GTG GTG GAG GAT CAT CAG GAG GTT CTA CCC TTT ATA   156
Leu Pro Val Trp Val Val Glu Asp His Gln Glu Val Leu Pro Phe Ile
            -85   -80   -75

TAC CGG GCC ATA GGC TCA AAG CAT CTT CCT GCC AGT AAT GTA AGT TTT   204
Tyr Arg Ala Ile Gly Ser Lys His Leu Pro Ala Ser Asn Val Ser Phe
            -70   -65   -60

TTA CAT TTC GAC TCA CAT CCA GAC CTC CTT ATT CCT GTG AAT ATG CCA   252
Leu His Phe Asp Ser His Pro Asp Leu Leu Ile Pro Val Asn Met Pro
        -55   -50   -45

GCA GAC ACC GTG TTT GAT AAG GAA ACA CTC TTT GGA GAA TTA AGT ATT   300
Ala Asp Thr Val Phe Asp Lys Glu Thr Leu Phe Gly Glu Leu Ser Ile
-40   -35   -30   -25

GAA AAT TGG ATT ATG CCT GCA GTT TAT GCT GGC CAT TTT TCA CAT GTA   348
Glu Asn Trp Ile Met Pro Ala Val Tyr Ala Gly His Phe Ser His Val
            -20   -15   -10

GTA TGG TTT CAT CCC ACA TGG GCT CAG CAG ATC AGA GAG GGC AGA CAC   396
Val Trp Phe His Pro Thr Trp Ala Gln Gln Ile Arg Glu Gly Arg His
            -5   1   5

CAC TTT   402
His Phe
    10

(2) INFORMATION FOR SEQ ID NO: 80:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 338 base pairs

```
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 12..152
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.3
                                   seq SSCVLLTALVALA/AY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:
```

```
AAAACGCGTG A ATG AGT AGC TGC CGC GGG CAG AAA GTT GCC GGA GGT CTC     50
           Met Ser Ser Cys Arg Gly Gln Lys Val Ala Gly Gly Leu
           -45                 -40                         -35

CGG GTG GTA TCG CCC TTT CCT CTT TGC CAG CCC GCT GGC GAG CCG AGC     98
Arg Val Val Ser Pro Phe Pro Leu Cys Gln Pro Ala Gly Glu Pro Ser
               -30                 -25                 -20

CGG GGC AAG ATG AGG TCG TCC TGT GTC CTG CTC ACC GCC CTG GTG GCG    146
Arg Gly Lys Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala
           -15                 -10                 -5

CTG GCC GCC TAT TAC GTC TAC ATC CCG CTG CCT GGC TCC GTG TCC GAC    194
Leu Ala Ala Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp
       1                   5                   10

CCC TGG AAG CTG ATG CTG CTG GAC GCC ACT TTC CGG GGT GCA CAS MMD    242
Pro Trp Lys Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Xaa Xaa
15                  20                  25                  30

NTA AGT RAC CTG GTC CAS TAC CTG GGA CTG AGC SRT CAC CTG CTG GCA    290
Xaa Ser Xaa Leu Val Xaa Tyr Leu Gly Leu Ser Xaa His Leu Leu Ala
           35                  40                  45

CTG ANN WTA WNA TTG TTT CTT TTG GCA AAA AAA GCG CGT GGT CTT CTG    338
Leu Xaa Xaa Xaa Leu Phe Leu Leu Ala Lys Lys Ala Arg Gly Leu Leu
       50                  55                  60
```

```
(2) INFORMATION FOR SEQ ID NO: 81:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 229 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
```

         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: 14..139
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION: score 6.1
                                   seq DLAVALSLLPAWT/ES

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATTAAAGTCA AAG ATG ATT ATT CCT TTC AAA ATA AAG AAT CTA GGA GGG   49
            Met Ile Ile Pro Phe Lys Ile Lys Asn Leu Gly Gly
               -40   -35

CGA GTC CTG CTG TCG GGA AGG GAG ATG TTT CCT GCT TCC GTC CGT GCT   97
Arg Val Leu Leu Ser Gly Arg Glu Met Phe Pro Ala Ser Val Arg Ala
-30   -25   -20   -15

CCT GAC CTG GCG GTG GCC CTG TCC CTG CTA CCT GCG TGG ACA GAG TCT   145
Pro Asp Leu Ala Val Ala Leu Ser Leu Leu Pro Ala Trp Thr Glu Ser
            -10   -5   1

CCA ACA CGC GGC AGC CAC CAG AGC CAG GCC CGA GCG CAC AGC CGT GCA   193
Pro Thr Arg Gly Ser His Gln Ser Gln Ala Arg Ala His Ser Arg Ala
            5   10   15

TTG CGA AAG CAA AGC CGA AAC ACG AGG TCG CCC CGG   229
Leu Arg Lys Gln Ser Arg Asn Thr Arg Ser Pro Arg
    20   25   30

(2) INFORMATION FOR SEQ ID NO: 82:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 249 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: 70..228
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION: score 6
                                   seq ALILLLLAQKGPS/XF

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ACGTAAAAC AGGTAGTTAC AAGGAGTGTC TTGATAATGA AATTTGTGGT ATAGAGTACT   60

```
GGTGAATGT ATG GTG TGT AGT GCT CCT AGA AAA ATA GTA GTT AGG GCA TTT    111
          Met Val Cys Ser Ala Pro Arg Lys Ile Val Val Arg Ala Phe
              -50               -45               -40          .

ATT ACG ATA ATA TTC ATA TAT TAT GCT ATA AAG AAG AGG GCA AAT GAA      159
Ile Thr Ile Ile Phe Ile Tyr Tyr Ala Ile Lys Lys Arg Ala Asn Glu
            -35               -30               -25

CCT GCA GCA TAT TTG ATG TTG AAG CCT GAG GCT CTG ATT CTC CTT CTG      207
Pro Ala Ala Tyr Leu Met Leu Lys Pro Glu Ala Leu Ile Leu Leu Leu
            -20               -15               -10

TTA GCT CAA AAG GGC CCC AGT HAG TTT CTG TTA GTG TGG AGA              249
Leu Ala Gln Lys Gly Pro Ser Xaa Phe Leu Leu Val Trp Arg
        -5                1                 5
```

(2) INFORMATION FOR SEQ ID NO: 83:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 289 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 110..229
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.9
                       seq VCSALCSLGEVRP/XE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```
ACCCTGCTGG GCGGGAAGGC GGCGCCCCGG CCGAGGTGGC GGCGGCTCCT CAGATGGGAG     60

AAGAAGTTGT CCATGTTCAC ACTGGGTGAA GGAAGCTGAA ACCACAGAC ATG ACT GAG    118
                                                       Met Thr Glu
                                                       -40

TCC TCC ATG AAG AAG CTG GCC TCC ACC CTG CTG GAC GCC ATC ACC GAT      166
Ser Ser Met Lys Lys Leu Ala Ser Thr Leu Leu Asp Ala Ile Thr Asp
        -35               -30               -25

AAG GAC CCC CTG GTG CAG GAG CAG GTC TGC AGT GCC CTG TGC TCC CTC      214
Lys Asp Pro Leu Val Gln Glu Gln Val Cys Ser Ala Leu Cys Ser Leu
        -20               -15               -10

GGG GAG GTG CGG CCV VTG GAG ACG CTC CGT GCC TGC GAG GAG TAT CTG      262
Gly Glu Val Arg Pro Xaa Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
    -5                1                 5                 10

CGG CAS ATG ACA AGC TGG CAC ACC CGG                                  289
```

Arg Xaa Met Thr Ser Trp His Thr Arg
        15   20

(2) INFORMATION FOR SEQ ID NO: 84:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 252 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 76..204
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.9
                                    seq VFLFHCTSGLSSC/KC

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AGTARAACAA AAGGATATGC ACACACACAT ATTTAAATAC ATGTAGTTTT TTGCATAAAT   60

TATCACTGAG AGGAA ATG CAA GAA ACT GAT TGT AAT AAA CGC TGG GGA AGG   111
              Met Gln Glu Thr Asp Cys Asn Lys Arg Trp Gly Arg
                       -40   -35

GGC CTG GGT GGC CTG TGG TCA GAA ACA GGA AGG AGA TTT CAT TGC AAA   159
Gly Leu Gly Gly Leu Trp Ser Glu Thr Gly Arg Arg Phe His Cys Lys
    -30   -25   .   -20

TCT TTT GTA TTT CTT TTT CAC TGT ACT TCT GGA TTA TCT TCA TGC AAA   207
Ser Phe Val Phe Leu Phe His Cys Thr Ser Gly Leu Ser Ser Cys Lys
-15   -10   -5   1

TGT TCT AAA AAG CAT TYM AAA TAT TGC TTC TGT TTT GTG GCA AGT   252
Cys Ser Lys Lys His Xaa Lys Tyr Cys Phe Cys Phe Val Ala Ser
            5   10   15

(2) INFORMATION FOR SEQ ID NO: 85:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 366 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 232..282
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 5.8
                          seq VPWLSSTVSCAQG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

ATGAGTGGTC MGGAGATAAC ACTTAATGCT TTATTCTTAA GTGTTGGAAG GAGCAAGTAA   60

GTGGTCTAGT GAGCTGTTTT TAGAGGAACT GTATAATATG TAACACATTG TCATTATATT   120

CACTAACTCC CAAAGTATTC TTGAGATATT GANACAAAAC AAAGAGCTTG AATAGAAACC   180

CTGAGCAACA ATGTATTTAC TTTCCACTTG CAGCAGAACT TGGCCTTTCA G ATG CTC   237
                                                         Met Leu

CTT GAA GTG CCT TGG CTT AGC AGT ACT GTC TCT TGT GCC CAG GGT CTG   285
Leu Glu Val Pro Trp Leu Ser Ser Thr Val Ser Cys Ala Gln Gly Leu
-15   -10   -5   1

AGA TTG GCA CAA CAC AGA GTG CCT TTC TTT TAT TCA AAT GTC TCA TTA   333
Arg Leu Ala Gln His Arg Val Pro Phe Phe Tyr Ser Asn Val Ser Leu
              5   10   15

TGC AAA TTA TTG CTG CCA GCC AMM CTG CAC GGG   366
Cys Lys Leu Leu Leu Pro Ala Xaa Leu His Gly
         20   25

(2) INFORMATION FOR SEQ ID NO: 86:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 437 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 123..209
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.7
                              seq SPAFLAVAGPGWA/RP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AACTCTCCCA TGCTGGTCTG TGGGGACTCC ATGTCCAAAC ACGCAGATCC TGCCTCCCAG   60

GCTTTAATTG ATCCTGCTGC CCTCTGGGAG CACCCACACA AGCCAGGCTC TCACTGGACC   120

TC ATG TCT GGA GGG CGG ATG CAG GCA CGG TGC TCC CAG CAA AGC ACC   167
   Met Ser Gly Gly Arg Met Gln Ala Arg Cys Ser Gln Gln Ser Thr
            -25   -20   -15

TGG AGT CCT GCC TTC CTT GCA GTG GCC GGG CCG GGC TGG GCA CGT CCT   215
Trp Ser Pro Ala Phe Leu Ala Val Ala Gly Pro Gly Trp Ala Arg Pro
            -10   -5   1

GGC TGT DCC CTG AGG ACC AAG TAT GAC TCT CAG CTG GCC CGG CAC CTC   263
Gly Cys Xaa Leu Arg Thr Lys Tyr Asp Ser Gln Leu Ala Arg His Leu
         5   10   15

TTG CAG CCT CAG TTC CCT GGT CTG ACC CTT GGG ACC CTG GTG CAA CCT   311
Leu Gln Pro Gln Phe Pro Gly Leu Thr Leu Gly Thr Leu Val Gln Pro
    20   25   30

GCC CAC TGG GGC ATG GGA GGG GGC ACA GGA GGG GTC TTG GGC GAG GGA   359
Ala His Trp Gly Met Gly Gly Gly Thr Gly Gly Val Leu Gly Glu Gly
35   40   45   50

GGG GGG CAC AGC TAT GCA GAG CAT GGC ACC TGC CTC CAG TCG TGC TCC   407
Gly Gly His Ser Tyr Ala Glu His Gly Thr Cys Leu Gln Ser Cys Ser
            55   60   65

ACA GAC GTG CTD ANG CAT GTC CTC CTG GCG   437
Thr Asp Val Leu Xaa His Val Leu Leu Ala
            70   75

(2) INFORMATION FOR SEQ ID NO: 87:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 437 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 63..116
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.6
                                     seq WHFLASFFPRAGC/HG

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AACTGTGGTC ACATCCCTCA AAAGTGAACA GTCGCCATCG GAGGCGTTTG GAGGAGACCG   60

TG ATG TTG CAG ATG CTG TGG CAT TTC CTA GCT AGC TTT TTC CCC AGG   107
   Met Leu Gln Met Leu Trp His Phe Leu Ala Ser Phe Phe Pro Arg
            -15   -10   -5

```
GCT GGG TGC CAC GGC TCC AGA GAG GGG GAC GAT CGT GAA GTC AGA GGC       155
Ala Gly Cys His Gly Ser Arg Glu Gly Asp Asp Arg Glu Val Arg Gly
            1                  5              10

ACC CCA GCC CCT GCC TGG AGA GAC CAG ATG GCA AGC TTT TTG GGG AAA       203
Thr Pro Ala Pro Ala Trp Arg Asp Gln Met Ala Ser Phe Leu Gly Lys
        15                  20              25

CAG GAC GGA AGG GCT GAG GCC ACG GAA AAA AGA CCC ACC ATT TTG CTG       251
Gln Asp Gly Arg Ala Glu Ala Thr Glu Lys Arg Pro Thr Ile Leu Leu
    30                  35              40                  45

GTG GTT GGA CCT GCA GAG CAG TTT CCT AAG AAA ATT GTA CAA GCT GGA       299
Val Val Gly Pro Ala Glu Gln Phe Pro Lys Lys Ile Val Gln Ala Gly
                50                  55              60

GAT AAG GAC CTT GAT GGG CAG CTA GAC TTT GAA GAA TTT GTC CAT TAT       347
Asp Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr
                65                  70              75

CTC CAA GAT CAT GAG AAG AAG CTG AGG CTG GTG TTT AAG AGT TTG GAC       395
Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp
            80                  85              90

AAA AAG AAT GAT GGA CGC ATT GAC GCG CAG GAG ATC ATG CAG             437
Lys Lys Asn Asp Gly Arg Ile Asp Ala Gln Glu Ile Met Gln
        95                  100             105
```

(2) INFORMATION FOR SEQ ID NO: 88:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 113 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 3..62
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 5.6
                            seq SLVCLLAMGKGLG/SS

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
AC ATG TAT TCC CAT CCC GTG TCC TCA CTG GTG TGT CTC CTG GCC ATG        47
   Met Tyr Ser His Pro Val Ser Ser Leu Val Cys Leu Leu Ala Met
   -20              -15              -10

GGC AAG GGA CTC GGG TCA TCC CAG GCC CTG GTC CAG CCA GAC ACC TGG       95
Gly Lys Gly Leu Gly Ser Ser Gln Ala Leu Val Gln Pro Asp Thr Trp
```

```
    -5                      1                  5                    10
CCC CAC ACC TCC CCG CGG                                             113
Pro His Thr Ser Pro Arg
            15
```

(2) INFORMATION FOR SEQ ID NO: 89:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 362 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

     (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 87..191
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.6
                        seq FIFMEVLGSGAFS/EV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
AACAGACCTG TACGAGCTGG AGTGGGAGCT CAAGCAGGAT TCTTCCCGAG TCCCTGGCAT    60

CCTCAGAAGC TTCAACTCTG GAGGCA ATG GGT CGA AAG GAA GAA GAT GAC TGC    113
                            Met Gly Arg Lys Glu Glu Asp Asp Cys
                            -35                 -30

AGT DCC TGG AAG AAA CAG ACC ACC AAC ATC CGG AAA ACC TTC ATT TTT    161
Ser Xaa Trp Lys Lys Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe
    -25             -20                 -15

ATG GAA GTG CTG GGA TCA GGA GCT TTC TCA GAA GTT TTC CTG GTG AAG    209
Met Glu Val Leu Gly Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys
-10              -5                  1                   5

CAA AGA CTG ACT GGG AAG CTC TTT GCT CTG AAG TGC ATC AAG AAG TCA    257
Gln Arg Leu Thr Gly Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser
            10              15                  20

CCT GCC TTC CGG GAC AGC AGC CTG GAG AAT GAG ATT GCT GTG TTG AAA    305
Pro Ala Phe Arg Asp Ser Ser Leu Glu Asn Glu Ile Ala Val Leu Lys
        25              30                  35

AAG ATC AAG CAT GAA AAC ATT GTG ACC CTG GAG GAC ATC TAT GAG AGC    353
Lys Ile Lys His Glu Asn Ile Val Thr Leu Glu Asp Ile Tyr Glu Ser
    40              45                  50

ACA CAA GGG                                                         362
Thr Gln Gly
55
```

(2) INFORMATION FOR SEQ ID NO: 90:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 384 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 241..327
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.6
                         seq LLPNQSLFSLARA/VR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
AAGCGGCGCA CCGGGHGAAG ATGGCGTTGG AGGTCGGCGA TATGGAAGAT GGGCAGCTTT   60

CCGACTCGGA TTCCGACATG ACGGTCGCAC CCAGCGACAG GCCGCTGCAA TTGCCAAAAG   120

TGCTAGGTGG CGACAGTGCT ATGAGGGCCT TCCAGAACAC GGCAACTGCA TGTGCACCAG   180

TATCACATTA TCGAGCTGTT GAAAGTGTGG ATTCAAGTGA AGAAAGTTTT TCTGATTCAG   240

ATG ATG ATA GCT GTC TTT GGA AAC GCA AAC GAC AGA AAT GTT TTA ACC   288
Met Met Ile Ala Val Phe Gly Asn Ala Asn Asp Arg Asn Val Leu Thr
            -25             -20             -15

CTC CTC CCA AAC CAG AGC CTT TTC AGT TTG GCC AGA GCA GTC AGA AAC   336
Leu Leu Pro Asn Gln Ser Leu Phe Ser Leu Ala Arg Ala Val Arg Asn
        -10             -5               1

CAC CTG TTG CTG GAG GAA AGA AGA TTA ACA ACA TAT GGG GTG CTG TGC   384
His Leu Leu Leu Glu Glu Arg Arg Leu Thr Thr Tyr Gly Val Leu Cys
    5               10              15
```

(2) INFORMATION FOR SEQ ID NO: 91:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 314 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

```
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 141..197
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 5.6
                                 seq LVVTAWFFGMCRS/KA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:


ATCCCAGAAC ACCATTGGGA GAACGCCAGG ACACCGTGAA GGCTGAGCCG CCACTCGGTT       60

CTGATGCCGC ATCCATTGGT CAGTGCACGT TCTTTGAGCT TCCACTTGAG TGCACGTTCT      120

TTGAGCTTCC ACTTGAGTGC ATG TTC TTT GAG CTT CCA CTT GTA GTG ACT GCC     173
                      Met Phe Phe Glu Leu Pro Leu Val Val Thr Ala
                                    -15                 -10

TGG TTC TTC GGG ATG TGC AGG AGC AAA GCG CTC TTA GGC AAT GCT CGT       221
Trp Phe Phe Gly Met Cys Arg Ser Lys Ala Leu Leu Gly Asn Ala Arg
             -5                   1                 5

TCT GCC CTG TGT TTA CAA ACC AAG GCC TGT GCC AGC TCT ACT CAG CCT       269
Ser Ala Leu Cys Leu Gln Thr Lys Ala Cys Ala Ser Ser Thr Gln Pro
    10                  15                  20

GAC ACC CAT AAT GAG CAC CAT CCC AGG AAT CCC TGT CCC TAC TTG           314
Asp Thr His Asn Glu His His Pro Arg Asn Pro Cys Pro Tyr Leu
    25                  30                  35



(2) INFORMATION FOR SEQ ID NO: 92:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 316 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 155..286
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 5.5
                                     seq FLLIVANVHFSQT/WV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:


ATAAATAGCA TTGTTTACAT CGACCAAATA TTGCCTGTTT CCTTTAATTC AAATGCATTA       60

GGTTCCCGCC TCCCTCTCCT TCCCCGCCAT GTTGCTGTTT TAAGGCTTCA TATGTATTAA      120
```

```
CATTTCTCTG ATCAAAATTG TGGCTGTTTT CCTT ATG AAC CAT AAT ATA ATC ATT   175
                                       Met Asn His Asn Ile Ile Ile
                                                              -40

TGT GTG ATG TAC ATT GTG CCA TTT TTG ATG ACT AAA TGT CTA TAT TTC     223
Cys Val Met Tyr Ile Val Pro Phe Leu Met Thr Lys Cys Leu Tyr Phe
        -35             -30             -25

TGC CAT TCC TGT AAG AGA GGG AGT TTT TTA CTG ATA GTA GCA AAT GTT     271
Cys His Ser Cys Lys Arg Gly Ser Phe Leu Leu Ile Val Ala Asn Val
    -20         .     -15             -10

CAC TTC AGT CAA ACT TGG GTG TTC AGT GGT AAA CCA TAT AAA GGG         316
His Phe Ser Gln Thr Trp Val Phe Ser Gly Lys Pro Tyr Lys Gly
-5                  1           5                  10
```

(2) INFORMATION FOR SEQ ID NO: 93:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 405 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 247..309
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.5
                                seq LTGLCXCCLQALG/LA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
ATTGTCTTAG TCCCATCCTC TGTTCCCCTG GCCAGTTTGT CTAGCTGTGT GGTCTCTGTT   60

CTCTCCCTAC CGTGCCTTCC ATCCCAGCCA TCCCTGACTA CGTGTTTCCC CCACAGACAT  120

CACACTGGTT CACCTCGTTG ACCACCGTTT CCTTCTCCCC AAGTCTCCCG GGCAAGGGCT  180

GATTCTCCAG TCTCCTCTGG GAAGCTGGCC CTGAACCACT TAGAACCTAT CGCTCCTTCG  240

TCACCT ATG TCA TGT GGC AGC GCT GCC TCA CTT ACG GGT CTG TGT KSG     288
       Met Ser Cys Gly Ser Ala Ala Ser Leu Thr Gly Leu Cys Xaa
       -20             -15             -10

TGC TGC CTC CAA GCC CTG GGG CTT GCG TGG CGC CGT CGC GGT TTG ACG    336
Cys Cys Leu Gln Ala Leu Gly Leu Ala Trp Arg Arg Arg Gly Leu Thr
-5                  1           5

GGA CCG GGC CTC CCC CCT GTG TTG CAG ATA TGC TGT CCA AGG AGC CTC    384
Gly Pro Gly Leu Pro Pro Val Leu Gln Ile Cys Cys Pro Arg Ser Leu
```

```
        10                    15              20              25
CGT GGT GTG ACG GCT CCT ACT                                            405
Arg Gly Val Thr Ala Pro Thr
            30
```

(2) INFORMATION FOR SEQ ID NO: 94:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 302 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 99..236
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.4
                         seq VLFFVGLITNGLA/MR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```
AAAAATACCA GATGCCACTC TGCAGGCTGC AATAACTACT ACTTACTGGA TACATTCAAA     60

CCCTCCAGAA TCAACAGTTA TCAGGTAACC AACAAGAA ATG CAA GCC GTC GAC AAC     116
                                           Met Gln Ala Val Asp Asn
                                                        -45

CTC ACC TCT GCG CCT GGG AAC ACC AGT CTG TGC ACC AGA GAC TAC AAA       164
Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr Arg Asp Tyr Lys
-40               -35             -30                 -25

ATC ACC CAG GTC CTC TTC CCA CTG CTC TAC ACT GTC CTG TTT TTT GTT       212
Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val Leu Phe Phe Val
            -20             -15                 -10

GGA CTT ATC ACA AAT GGC CTG GCG ATG AGG ATT TTC TTT CAA ATC CGG       260
Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe Phe Gln Ile Arg
            -5              1               5

AGT AAA TCA AAC TTT ATT ATT TTT CTT AAG AAC ACA GTS AAG               302
Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr Val Lys
       10              15              20
```

(2) INFORMATION FOR SEQ ID NO: 95:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 99 base pairs
        (B) TYPE: NUCLEIC ACID

```
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

     (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 16..75
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.3
                                    seq LCSSCCSWGPAAG/AL

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:
```

```
AGAAGTAGCC GCAGG ATG GCG GCG GCT ATG CSS TTG CTC TGC TCG TCC TGT        51
                 Met Ala Ala Ala Met Xaa Leu Leu Cys Ser Ser Cys
                 -20                 -15                 -10

TGC TCC TGG GGC CCG GCG GCT GGT GCC TTG CAG AAC CCC CAA CGC GGG        99
Cys Ser Trp Gly Pro Ala Ala Gly Ala Leu Gln Asn Pro Gln Arg Gly
         -5                     1                 5
```

```
(2) INFORMATION FOR SEQ ID NO: 96:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 485 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

     (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 396..470
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.3
                                    seq SVVKVLSLRKAQA/QS

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:
```

```
ATTTCTGCCC ACGGGCATAA GTTCAAAAGA AAGCTGCGAA AAGTTGGAGA CTGCTGATGA        60

AACCAGTCAT CTCCAGCCAC TCAACAAGCG TCAGAGGACA AGCTCTGTGG TGGAAGAGCA       120

TTTCCAAGCC TCAGTATCTC CCACTGAAGC CGCACCCCCT GCCACAGGAG ACCAGAGTCC       180

TGGCCTGGGC ACCCAGCCAA AGCTGCCATC CAGCAGTGGC CTTCCTGCTG CAGACGTGTC       240
```

CCCTGCCACA GCTGAAGAGC CCTTGTCACC TTCCACACCC ACCCGCCGGC CTCCCTTCAC   300

CCGAGGGCGA CTCCGGCTGC TCTCCTTTCG ATCCATGGAG GAGGCCAGAC TGGTGCCCAC   360

AGTGAAAGAS CAAATACCCT GTGCTGAAGG ACGTC ATG GAC TTC ATT AAG GAT   413
                                       Met Asp Phe Ile Lys Asp
                                       -25   -20

CAG TCG CTC TCG CAC AGG AGT GTT GTG AAG GTT CTT TCC CTG AGG AAA   461
Gln Ser Leu Ser His Arg Ser Val Val Lys Val Leu Ser Leu Arg Lys
            -15   -10   -5

GCC CAG GCC CAG AGC ATC CTG GAA   485
Ala Gln Ala Gln Ser Ile Leu Glu
            1   5

(2) INFORMATION FOR SEQ ID NO: 97:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 283 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 59..142
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.3
                                    seq RISCAFSLASSTA/RQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AGTGTGTGAA GCGTACCTAR GGCGGGAGGC GACATGGWGA CAGGGGCGGY CGWGCTGT   58

ATG ACC AGG CCC TTT TGG GCA TCC TGC AGC ACG TGG GCA ACG TCC AGG   106
Met Thr Arg Pro Phe Trp Ala Ser Cys Ser Thr Trp Ala Thr Ser Arg
        -25   -20   -15

ATT TCC TGC GCG TTC TCT TTG GCT TCC TCT ACC GCA AGA CAG ACT TCT   154
Ile Ser Cys Ala Phe Ser Leu Ala Ser Ser Thr Ala Arg Gln Thr Ser
        -10   -5   1

ATC GCT TGC TGC GCC ACC CAT CGG ACC GCA TGG GCT TCC CGC CCG GGG   202
Ile Ala Cys Cys Ala Thr His Arg Thr Ala Trp Ala Ser Arg Pro Gly
5   10   15   20

CCG CGC AGG CCT TGG TGC TGC AGG TAT TCA AAA CCT TTG ACC ACA TGG   250
Pro Arg Arg Pro Trp Cys Cys Arg Tyr Ser Lys Pro Leu Thr Thr Trp
            25   30   35

CCC GTC AGG ATG ATG AGA AGA GAA GGC AGY KGA   283

Pro Val Arg .Met Met Arg Arg Glu Gly Ser Xaa
        40   45

(2) INFORMATION FOR SEQ ID NO: 98:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 390 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 286..333
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.3
                                     seq CAVSLTTAAVAFG/DE

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ACTNTGTGCT GGTGCTGGCA AAGTTTGTGA TTTTAAGAAA TTCTGCTGTG CTCTCCAGCA   60

CTGCGAGCTT CTGCCTTCCC TGTAGTTTCC CAGATGTGAT CCAGGTAGCC GAGATTCCGC   120

TGCCCGTGCT TCGGTAGCTT AAGTCTTTGC CTCAGCTTTT TTCCTTGCAG CCGCTGAGGA   180

GGCGATAAAA TTGGCGTCAC AGTCTCAAGC AGCGATTGAA GGCGTCTTTT CAACTACTCG   240

ATTAAGGTTG GGTATCGTCG TGGGACTTGG AAATTTGTTG TTTCC ATG AAA TCC TGC   297
                                               Met Lys Ser Cys
                                                      -15

GCA GTG TCG CTC ACT ACC GCC GCT GTT GCC TTC GGT GAT GAG GCA AAG   345
Ala Val Ser Leu Thr Thr Ala Ala Val Ala Phe Gly Asp Glu Ala Lys
        -10   .-5   1

AAA ATG GCG GAA GGA AAA GCG AGC CGC GAG AGT GAA GAG GAG ACG   390
Lys Met Ala Glu Gly Lys Ala Ser Arg Glu Ser Glu Glu Glu Thr
  5   ·   10   15

(2) INFORMATION FOR SEQ ID NO: 99:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 254 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

(ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 138..200
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.2
                                 seq LSLSLICLRMSLS/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATGTGATTWT KTTCCTATTT ATTTTAAATA CACACACCCA CAGGGCTCTG CCCCTGTAAA   60

AGAAAAAAAA TCAAAACAAA CAAATAAATA ACCCCAAAGA GATGGACCCA GGGGAGAACG   120

CGTAAGTRTG AAGGGGC ATG AGT ATA CAC GAG TGT GCG TGT CTT TCC CTC   170
                    Met Ser Ile His Glu Cys Ala Cys Leu Ser Leu
                    -20   -15

TCC CTT ATT TGT CTC CGT ATG AGT CTC TCC TTG TAC CCT CCC CCT GCC   218
Ser Leu Ile Cys Leu Arg Met Ser Leu Ser Leu Tyr Pro Pro Pro Ala
-10   -5   1   5

TCG ATG ATA TTA CTC CCC CAG ACT TGG AAG CCG CGC   254
Ser Met Ile Leu Leu Pro Gln Thr Trp Lys Pro Arg
        10   15

(2) INFORMATION FOR SEQ ID NO: 100:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 303 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 178..222
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 5.2
                                         seq SGLSFLSVFSLWC/EP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGATCTRGA ARCAGTRACC CTCTCTCTTT GCATRAGTTT CTCTTTTTTC TCTGAGTTAC   60

AGTTTTGARR RCAGCWRCTA ATTTTTTTAA TCCCTCGAAT AACTCAGTTT TAGGAACATT   120

CGCTCTCCCT AAGCCTTACC TTGAAACCAG TGTAGGATTT TGCTGCCACC CCGGAAG   177

```
ATG CTG AGT GGA CTC AGC TTC CTA TCC GTT TTC TCC CTC TGG TGT GAG    225
Met Leu Ser Gly Leu Ser Phe Leu Ser Val Phe Ser Leu Trp Cys Glu
-15             -10             -5                          1

CCC ACA CTC CCG GCG CTG GGA AAT GGC TCT GTT CTA GGA GTG CGG CWR    273
Pro Thr Leu Pro Ala Leu Gly Asn Gly Ser Val Leu Gly Val Arg Xaa
            5               10              15

TCA TCC TCT TCC TCT GCC CAG TGC TCT CTG                            303
Ser Ser Ser Ser Ser Ala Gln Cys Ser Leu
        20              25
```

(2) INFORMATION FOR SEQ ID NO: 101:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 380 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 120..374
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.2
                          seq LYSILHFPFWVHG/RX

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
AACTTTGATG GAATCAAAGG TCATGGGCGC CAGGGCAGCT GTTCCCACAT GCAGGTGGGG    60

GCCCGCCCTT TGTTCACACC TACATTCAAG GAATTCTGTT GGGCTCATAA TTCGTTGTG    119

ATG GGG TTA AAG GAC AAA TCT CAG GCC CCC GCC TCA GGA CTG GGA GTT    167
Met Gly Leu Lys Asp Lys Ser Gln Ala Pro Ala Ser Gly Leu Gly Val
-85             -80             -75                         -70

CTC CGA GGG CAA AGG TCG GGC TCA TTC ATT TCT ATG CCT GCC CCA GCC    215
Leu Arg Gly Gln Arg Ser Gly Ser Phe Ile Ser Met Pro Ala Pro Ala
            -65             -60             -55

TCA GGC CAG TKC CCG GAA GAA AGC AGG TCC CCA GCT CCA CCA GTG GCT    263
Ser Gly Gln Xaa Pro Glu Glu Ser Arg Ser Pro Ala Pro Pro Val Ala
            -50             -45             -40

TCT AGG TCT CAG AAC AGA GGC TAC AGA CCG TGG CAT GGG CCC CTT TGG    311
Ser Arg Ser Gln Asn Arg Gly Tyr Arg Pro Trp His Gly Pro Leu Trp
        -35             -30             -25

GTC CAC CAA AGT GTT CGG TTT GGA CTT TAC AGC ATT TTG CAT TTT CCT    359
Val His Gln Ser Val Arg Phe Gly Leu Tyr Ser Ile Leu His Phe Pro
```

```
        -20                    -15                    -10

TTT TGG GTT CAC GGC CGA YAG                                              380
Phe Trp Val His Gly Arg Xaa
 -5                        1
```

(2) INFORMATION FOR SEQ ID NO: 102:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 265 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

     (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 65..193
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.2
                              seq PMQLLQVLSDVLA/EI

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```
AATGCCAGTA TTAAGGATTT TTTTTTCTAT TTTTACTCTT TAGTTAAAAT TATAAGACCT      60

AATT ATG AGT GAT CAA ATT AAA TTC ATT ATG GAC AGT CTC AAT AAG GAG      109
     Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu
         -40                  -35                   -30

CCC TTT AGG AAG AAC TAT AAT TTA ATC ACG TTT GAT TCC TTG GAG CCA      157
Pro Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Asp Ser Leu Glu Pro
        -25                  -20                   -15

ATG CAA CTA TTA CAA GTT CTC AGT GAT GTT CTG GCT GAG ATT GAC CCA      205
Met Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro
        -10                   -5                    1

AAG GTA AGA GTT TTC TCT TTC TTT TTG ATG GGT AGC AGA AAG CCA ATT      253
Lys Val Arg Val Phe Ser Phe Phe Leu Met Gly Ser Arg Lys Pro Ile
 5                    10                   15                   20

TCT CCC TCT TGG                                                       265
Ser Pro Ser Trp
```

(2) INFORMATION FOR SEQ ID NO: 103:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 354 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE

            (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 25..336
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.1
                                    seq SSVASLTATPSLA/SP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAACCTTGTA CAACACCGGC CGAC ATG TCT CCT TCC TGC CTG CAC CCC GAC   51
                           Met Ser Pro Ser Cys Leu His Pro Asp
                                             -100

CTG TGG TCA ATG TGT CTG GAG GTC CCC TCC TTT ACA GCC ACC GAC TCA   99
Leu Trp Ser Met Cys Leu Glu Val Pro Ser Phe Thr Ala Thr Asp Ser
-95   -90   -85   -80

GTG AAC TGC GGC TGC TGT TTG GAG CTC GCG ACG GAG CCG GCT CGG AAC   147
Val Asn Cys Gly Cys Cys Leu Glu Leu Ala Thr Glu Pro Ala Arg Asn
                -75   -70   -65

ATC AGA TCA ACC ACC AGG GCT TCT CTG CTG AGG TGC AGC TCA TTC ACT   195
Ile Arg Ser Thr Thr Arg Ala Ser Leu Leu Arg Cys Ser Ser Phe Thr
            -60   -55   -50

TCA ACC AGG AAC TCT ACG GGA ATT TCA GCG CTG CCT CCC GCG GCC CCA   243
Ser Thr Arg Asn Ser Thr Gly Ile Ser Ala Leu Pro Pro Ala Ala Pro
            -45   -40   -35

ATG GCC TGG CCA TTC TCA GCC TCT TTG TCA ACG TTG CCA GTA CCT CTA   291
Met Ala Trp Pro Phe Ser Ala Ser Leu Ser Thr Leu Pro Val Pro Leu
    -30   -25   -20

ACC CAT TCC TCA GTC GCC TCC TTA ACC GCG ACA CCA TCA CTC GCA TCT   339
Thr His Ser Ser Val Ala Ser Leu Thr Ala Thr Pro Ser Leu Ala Ser
-15   -10   -5   1

CCT ACA AGA ATG ATG   354
Pro Thr Arg Met Met
            5

(2) INFORMATION FOR SEQ ID NO: 104:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 226 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Homo Sapiens
     (F) TISSUE TYPE: Brain

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 155..202
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 5.1
                             seq SFHLLLDPSSTQS/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

AACTCTGGAA TGAAGGGGGG AATTACGGGT TGGTGGTCGG CTTCATGTTA GGAGGACACC   60

CCTCCATCTG TTCACAGCTC AGCCTGTTTC CAATTTAAAG CCCAGAAGAA GCCTTCCCAG   120

CCTACTCAGA ATCCCACATC CTCTCCTCTC TCTT ATG GAT CTC AGT TTT CAT TTA   175
                                      Met Asp Leu Ser Phe His Leu
                                      -15   -10

TTA CTA GAT CCT TCC TCT ACT CAA TCA AGC ATA CTG AAG CAC CTC CCA   223
Leu Leu Asp Pro Ser Ser Thr Gln Ser Ser Ile Leu Lys His Leu Pro
          -5   1   5

TGT   226
Cys

(2) INFORMATION FOR SEQ ID NO: 105:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 447 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 289..366
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 5
                                 seq VISVLILVGFGAC/IY

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

ATCTCTGATG GGCAGGGAGA GATACCAGGG TGCTGAGCCA GTCCAGGACT GCCCCCTCCT   60

GGCCCACTCA GAGCCCCTGG GTGTGAGAAG CTCGTCTCCC GTGGGTTGCA TTGGCTCTGC   120

CCTATCTCTG CCTCCAGCAC CCAGGGCGGC CGCAGATGGC AGTGTCTCTG GGACAGCAG   180

CTGCGAATGA GTCCACGGGC CAACGCTGAG CTGCTCAGGC TGAGGCGGTG TGCTCAGCAC   240

AGAGCCCCCG GAACTGGCAT CTGCAGGGCG TGAGCCAARG CCGCCGCG ATG CCG CAC   297
                                                       Met Pro His
                                                       -25

TTC CTG GAC TGG TTC GTG MCG GTC TAC TTG GTC ATC TCG GTC CTC ATT   345
Phe Leu Asp Trp Phe Val Xaa Val Tyr Leu Val Ile Ser Val Leu Ile
            -20   -15   -10

CTG GTG GGC TTC GGC GCC TGC ATC TAC TAC TTC GAG CCG GGC CTG CAG   393
Leu Val Gly Phe Gly Ala Cys Ile Tyr Tyr Phe Glu Pro Gly Leu Gln
        -5   1   5

GAG GCG CAC AAG TGG CGC ATG YAG CGC CCC TGG TGG ACC GCG ACC TCC   441
Glu Ala His Lys Trp Arg Met Xaa Arg Pro Trp Trp Thr Ala Thr Ser
 10   15   20   25

ACT GGG   447
Thr Gly

(2) INFORMATION FOR SEQ ID NO: 106:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 195 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 79..168
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5
                                    seq IVGLLAQLEKINA/EP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AACAGAAAGA TGACTTAAAG AACGTGGGGA GTCGCTCGCA GTTCGATTAT CTGCAATTAT   60

GAAATGAAGT AACTCAAG ATG AGC AAG TTA AAA GTG ATA CCA GAA AAA AGC   111
                     Met Ser Lys Leu Lys Val Ile Pro Glu Lys Ser
                     -30   -25   -20

CTT ACC AAT AAT TCT AGG ATC GTA GGA CTC CTG GCT CAA CTG GAG AAG   159
Leu Thr Asn Asn Ser Arg Ile Val Gly Leu Leu Ala Gln Leu Glu Lys
            -15   -10   -5

ATC AAT GCT GAG CCT TCA GAA TCW GAC ACT AGC CGG   195
Ile Asn Ala Glu Pro Ser Glu Ser Asp Thr Ser Arg
             1   5

(2) INFORMATION FOR SEQ ID NO: 107:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 38..106
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5
                        seq LIPAMAFLSCVRP/ES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:


```
AACTGCTGCT CACAGAAGCA GTGAGGATGA TGCCAGG ATG ATG TCT GCC TCG CGC      55
                                            Met Met Ser Ala Ser Arg
                                                               -20

CTG GCT GGG ACT CTG ATC CCA GCC ATG GCC TTC CTC TCC TGC GTG AGA      103
Leu Ala Gly Thr Leu Ile Pro Ala Met Ala Phe Leu Ser Cys Val Arg
        -15             -10                 -5

CCA GAA AGC WGG GAG CCC TGC GTG GAG GTG GTT CCT AAT ATT ACT TAT      151
Pro Glu Ser Xaa Glu Pro Cys Val Glu Val Val Pro Asn Ile Thr Tyr
    1           5               10                      15

CAA TGC ATG GAG CTG                                                   166
Gln Cys Met Glu Leu
              20
```


(2) INFORMATION FOR SEQ ID NO: 108:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 278 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide

```
            (B) LOCATION: 84..230
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.9
                                    seq VTVCCXLVAFLFC/IL


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:


AARAGACTCC GCCCCCTTCC TTGGAGCGCC GCGNCTCGGG CTGAGGGAGC TCGGGCCAAT    60

CAGAGGGACG GCCCCAGART GGC ATG GTA GAT GGA ACG CAG CTG AGA GGT CTG   113
                        Met Val Asp Gly Thr Gln Leu Arg Gly Leu
                        -45                         -40

ACA AGA ATG TAC CAG GTC CCA CTA MCA CTG GAT CGG GAT GAG ACC CTG    161
Thr Arg Met Tyr Gln Val Pro Leu Xaa Leu Asp Arg Asp Glu Thr Leu
        -35                 -30                 -25

GTA CGG CTC CGC TTC ACC ATG GTG GCC CTG GTC ACG GTC TGC TGT MCA   209
Val Arg Leu Arg Phe Thr Met Val Ala Leu Val Thr Val Cys Cys Xaa
        -20                 -15                 -10

CTT GTC GCC TTC CTC TTC TGC ATC CTC TGG TCC CTG CTC TTC CAC TTC   257
Leu Val Ala Phe Leu Phe Cys Ile Leu Trp Ser Leu Leu Phe His Phe
    -5                  1                   5

AAG GAG ACA ACG GCC ACA GGG                                         278
Lys Glu Thr Thr Ala Thr Gly
10                  15




(2) INFORMATION FOR SEQ ID NO: 109:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 217 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

     (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 116..193
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.9
                                    seq LISMLQMLAVIIT/NT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:


ACTTGAAGTT CYYCTGGGGG CAATGAGATG GCAGCTATAC AGCGAGTCTG AAAAGAACAT    60

CCACATTCCT AATCCCTAGG AATATGATTA TTGGAAAATA GATATAATTA TACAA ATG    118
                                                                   Met
```

```
AAA CAG AAC TTC CTT GTT CTC AAC AGT GTC TGG TAC CTA ATA AGC ATG       166
Lys Gln Asn Phe Leu Val Leu Asn Ser Val Trp Tyr Leu Ile Ser Met
-25                 -20                 -15                 -10

TTA CAA ATG TTA GCT GTG ATC ATT ACC AAC ACC ACC ATC ACC ACC ATT       214
Leu Gln Met Leu Ala Val Ile Ile Thr Asn Thr Thr Ile Thr Thr Ile
             -5                  1                   5

GGG                                                                    217
Gly
```

(2) INFORMATION FOR SEQ ID NO: 110:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 426 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 55..231
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.9
                                    seq LVEMCLEVLGSSA/GD

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```
AATTCAGAAT TAGAAAACAA ACCAGTAGAT TTTTTGAAC AAAAATCTTT AGAA ATG        57
                                                            Met

GAA TGT CAA AAT AGT TCT TTA AAA AAG TGT TTA CTA GTT GAA AAG TCA       105
Glu Cys Gln Asn Ser Ser Leu Lys Lys Cys Leu Leu Val Glu Lys Ser
         -55                 -50                 -45

CTT GTG AAA GCT TCT TAT TTA ATT GCT TTC CAA ACT GCT GCA AGC AAG       153
Leu Val Lys Ala Ser Tyr Leu Ile Ala Phe Gln Thr Ala Ala Ser Lys
         -40                 -35                 -30

AAG CCA TTC TCB ATT GCT GAA GAA TTA ATT AAA CCA TAT TTA GTA GAA       201
Lys Pro Phe Ser Ile Ala Glu Glu Leu Ile Lys Pro Tyr Leu Val Glu
    -25                 -20                 -15

ATG TGT TTA GAA GTT TTG GGT TCA AGT GCT GGA GAC AAA ATG AAA ACT       249
Met Cys Leu Glu Val Leu Gly Ser Ser Ala Gly Asp Lys Met Lys Thr
-10                 -5                  1                   5

ATT CCA CTT TCT AAT GTT ACA ATT CAA CAC AGG ATT GAT GAA CTA TCT       297
Ile Pro Leu Ser Asn Val Thr Ile Gln His Arg Ile Asp Glu Leu Ser
             10                  15                  20

GCA GAC ATT GAA GAC CAG CTG ATT CAA AAG GTC AGA GAG TCA AAG TGG       345
```

```
Ala Asp Ile.Glu Asp Gln Leu Ile Gln Lys Val Arg Glu Ser Lys Trp
        25              30               35
```

```
TTT GCC CTT CAG ATA GAT GAG TCA TCA GAA ATC TCA AAT ATC ACA CTT    393
Phe Ala Leu Gln Ile Asp Glu Ser Ser Glu Ile Ser Asn Ile Thr Leu
        40              45               50
```

```
CTT TTG TGC TAT ATT CGT TTC ATT GAT TAT GAT                        426
Leu Leu Cys Tyr Ile Arg Phe Ile Asp Tyr Asp
55              60               65
```

(2) INFORMATION FOR SEQ ID NO: 111:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 95 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 15..83
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.8
                        seq VMWLVALLEMCVC/KK

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```
ATTGAAAAAT AAAA ATG CAC TCT AGT ATA AAA ACG AAG GGA AGC GTC ATG    50
                Met His Ser Ser Ile Lys Thr Lys Gly Ser Val Met
                            -20                 -15
```

```
TGG CTT GTT GCT CTT TTG GAG ATG TGT GTG TGT AAG AAG TCC AGG        95
Trp Leu Val Ala Leu Leu Glu Met Cys Val Cys Lys Lys Ser Arg
    -10             -5               1
```

(2) INFORMATION FOR SEQ ID NO: 112:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 473 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 342..395
         (C) IDENTIFICATION METHOD: .Von Heijne matrix
         (D) OTHER INFORMATION:  score 4.8
                                 seq LEAISSLSSFVLG/RM

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:


ACTGTTTATA GATATTTTGT TTCCCTGAGC AACAGAAAAT GCAGTGCTTA TTTAACTTAG   60

CAGCAATGCC TTGTAAAAAT ATAAGCCTGC AGATGGCAAT GGCCTCTATT TTTCTTCCAC  120

AAGTTTCTTC CAATTCAGAG CCCGTGCCTT CCTTCAGCCA CAGAGCGCAC AACAGCATGG  180

ATGAGATTGA GTCAGCCCTC TTACATTGTT GGCCTACAGC TATGGAGCTA CCTTTGCAGA  240

GTTGTCCACT TTGGGGTTTG AGCATGGGAA GTAAATTCAG AGATGCAAGT ATCTGGGAGA  300

GGGCATGAAC TCGTGAGAAA GTCCTCATAT TCTGAGCTCC T ATG ACA GTT TTG CCT  356
                                             Met Thr Val Leu Pro
                                                          -15

TTA GAA GCT ATC TCG TCT CTT AGC AGC TTT GTT TTG GGC AGA ATG AAT  404
Leu Glu Ala Ile Ser Ser Leu Ser Ser Phe Val Leu Gly Arg Met Asn
              -10             -5                     1

AGC AGA GGG GCA GGA AAG ACC CAG AAT CTT GAT GCC AGC TCC YTG CTT  452
Ser Arg Gly Ala Gly Lys Thr Gln Asn Leu Asp Ala Ser Ser Leu Leu
         5               10              15

TTA CTC TGC TGC TTG ATA CTG                                      473
Leu Leu Cys Cys Leu Ile Leu
 20              25




(2) INFORMATION FOR SEQ ID NO: 113:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 386 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 12..101
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.8
                                    seq ILFCVGAVGACTL/SV

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
```

```
AATACACAGA A ATG GGG ACT GCG AGC AGA AGC AAC ATC GCT CGC CAT CTG    50
              Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu
              -30               -25                 -20

CAA ACC AAT CTC ATT CTA TTT TGT GTC GGT GCT GTG GGC GCC TGT ACT    98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr
        -15               -10                 -5

CTC TCT GTC ACA CAA CCG TGG TAC CTA GAA GTG GAC TAC ACT CAT GAG    146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu
    1               5                 10                  15

GCC GTC ACC ATA AAG TGT ACC TTC TCC GCA ACC GGA TGC CCT TCT GAG    194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu
            20              25                  30

CAA CCA ACA TGC CTG TGG TTT CGC TAC GGT GCT CAC CAG CCT GAG AAC    242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn
            35              40                  45

CTG TGC TTG GAC GGG TGC AAA AGT GAG GCA GAS AAG TTC ACA GTG AGG    290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg
        50              55                  60

GAG GCC CTC AAA GAA AAC CAA GTT TCC CTC ACT GTA AAC AGA GTG ACT    338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr
        65              70              75

TCA AAT GAC AGT GCA ATT TAC ATC TGT GGA ATA GCA TTC CCC AGT GTA    386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
80              85              90                  95
```

(2) INFORMATION FOR SEQ ID NO: 114:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 147 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 10..84
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.8
                                  seq ALFYSVVVSTVSG/NE

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:


```
AAGAGTCTG ATG AAT AGC AGT AAA GAA GAA ATG CGC GAA CTG GCA GCG TTG    51
          Met Asn Ser Ser Lys Glu Glu Met Arg Glu Leu Ala Ala Leu
```

```
            -25                    -20                    -15
TTT TAT TCT GTA GTG GTA TCA ACA GTG TCG GGG AAT GAG TTG AAA TCA        99
Phe Tyr Ser Val Val Val Ser Thr Val Ser Gly Asn Glu Leu Lys Ser
    -10         •         -5                    1              5

ATG ATA GAA CAG CTT ATA AAG ACT ACA AAA GAC AAT CAC AGC CTA CGG      147
Met Ile Glu Gln Leu Ile Lys Thr Thr Lys Asp Asn His Ser Leu Arg
                10                    15                    20
```

(2) INFORMATION FOR SEQ ID NO: 115:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 297 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 55..210
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.7
                         seq LLAKALHLLKSSC/AP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```
AAGTTGTGCG CCGGTCCCTG GGCCTGAGCT CCGGCTCCGG CTGGGGCGCC TGCG ATG         57
                                                             Met

TCT CAA GAT GGC GGA STG GGC GAA TTA AAG CAC ATG GTG ATG AGT TTC       105
Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser Phe
    -50                 -45                 -40

CGG GTG TCT GAG CTC CAG GTG CTT CTT GGC TTT GCT GGC CGG AAC AAG       153
Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn Lys
 -35                 -30                 -25                 -20

AGT GGA CGG AAG CAC GAG CTC CTG GCC AAG GCT CTG CAC CTC CTG AAG       201
Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu Lys
                -15                 -10                 -5

TCC AGC TGT GCC CCT AGT GTC CAG ATG AAG ATC AAA GAG CTT TAC CGA       249
Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr Arg
                1              5                    10

CGA CGC TTT CCC CGG AAG ACC CTG GGG CCC TCT GAT CTC TCC TCC GGG       297
Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Ser Gly
        15                    20                    25
```

(2) INFORMATION FOR SEQ ID NO: 116:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 141 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 1..87
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.7
                        seq LCYLSIFCLGVLF/II

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:


```
ATG CCT TGT ATA TCT CTC TTA GGT CTA CTT TAT AAT TTT GTT CAA GTC    48
Met Pro Cys Ile Ser Leu Leu Gly Leu Leu Tyr Asn Phe Val Gln Val
        -25             -20             -15

CTC TGT TAC TTA TCG ATC TTC TGT CTA GGT GTT CTG TTC ATT ATT GAA    96
Leu Cys Tyr Leu Ser Ile Phe Cys Leu Gly Val Leu Phe Ile Ile Glu
        -10             -5                      1

CGT GGT TCA TTA AAA GTC TCC AAA TTA ATC TGT AGG CCA CCA GGG       141
Arg Gly Ser Leu Lys Val Ser Lys Leu Ile Cys Arg Pro Pro Gly
    5               10              15
```


(2) INFORMATION FOR SEQ ID NO: 117:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 307 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 167..211
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.7
                        seq IAVLFCFFLLIIF/QT

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

AACTAAGVWN KTTCAGCAAA TACTTTTCAA CATTCCCTTC TGTCCTTTCT TTGTTTTTAA   60

AGAAAGCTCT GATTTTGTTT CATTTTCAGC TGGAGACTTA AATGACACCA AGCAAAGCCT   120

ACTTAGTTTA GATCTCCAGA AATTGGCTGG TGGAAAAAAA TCAAAC ATG AAG ATT   175
                                                  Met Lys Ile
                                                  -15

GCA GTT TTG TTT TGT TTT TTT CTG CTT ATC ATT TTT CAA ACT GAC TTT   223
Ala Val Leu Phe Cys Phe Phe Leu Leu Ile Ile Phe Gln Thr Asp Phe
    -10   -5   1

GGA AAA AAT GAA GAA ATT CCT AGG AAG CAA AGG AGG AAG ATC TAC CAC   271
Gly Lys Asn Glu Glu Ile Pro Arg Lys Gln Arg Arg Lys Ile Tyr His
5   10   15   20

AGA AGG TTG AGG AAA AGT TCA ACC TCA CAC AAG CAG   307
Arg Arg Leu Arg Lys Ser Ser Thr Ser His Lys Gln
            25   30

(2) INFORMATION FOR SEQ ID NO: 118:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 396 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 253..381
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.7
                                  seq STWSSASLRGSWQ/QG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATACTGATG TCTYCCGAAA AACACAGCCC CAAGGGAGTC GAGACGWTGT ACCAGGTAGA   60

ATAAGGCACA GGGGAGCCGC TTGACAAATC AGACGACGGC AGCCGGCCTG CCTGCCCGGT   120

ATGTGGCCAA ATATGGGCGA GGCCAAGGTT GGGGTGTGAA AGTGCGTGAC GTTTACACCC   180

ACGTGGGCGT CTGTGCACGT GCGTGTGTGC GTGTGAGCTG CCTGTGGGCA TCTGCAGAAG   240

CAGACATTCT TC ATG GCT AAA CAA AAA CCT CAC GTT TTG GGT TCC AGG GTG 291
         Met Ala Lys Gln Lys Pro His Val Leu Gly Ser Arg Val
             -40   -35

ATG CCA GCG AGT TGT GTT TCT GAG AGA CGA AGG AAG CCT TCC TTC CAG   339
Met Pro Ala Ser Cys Val Ser Glu Arg Arg Arg Lys Pro Ser Phe Gln

```
-30                    -25                 -20                 -15
GTT TCC ACG TGG AGC AGT GCC TCT CTG CGT GGT TCC TGG CAG CAG GGG   387
Val Ser Thr Trp Ser Ser Ala Ser Leu Arg Gly Ser Trp Gln Gln Gly
                    -10                 -5                   1

ATG CCA GGC                                                        396
Met Pro Gly
         5
```

(2) INFORMATION FOR SEQ ID NO: 119:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 193 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 143..187
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.6
                          seq FLYLKSVFDVSLG/AR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```
ATGGAGATCC ATAACATGAT CCTACATGAA TGTTTCAATA TTGTATTCCT GTAAGTTACT   60

TTTACATTGA CAGTTCTGAA ATTCATGTTG AGTGTTAATT AGGCAGGAAA TCAGAAGGGA   120

GGTTTTGTAG AAGGTCGTAT CC ATG GGT TTT TTA TAT TTG AAA AGT GTT TTC   172
                        Met Gly Phe Leu Tyr Leu Lys Ser Val Phe
                        -15                 -10

GAT GTA TCA TTG GGG GCA AGG                                        193
Asp Val Ser Leu Gly Ala Arg
 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 120:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 460 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:

             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 254..436
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 4.6
                                    seq LLLLHGGGHSALS/WA

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AAGTTTACGG AGCCGGTGGG CGGTAGGCGG TGCTACGGGT AGCTGGGTGC TGTCCAAAGG   60

CGACAGGGCG TCGTTAGGGG AGCGAGTCGT GACCGGTTGG GCCACACTCA ACGTGGGACG   120

AAGCTTCGCC TACTGTTTGA CTACGTGCGT GCAGCCTCCC CTCGATGTCG GCCCTCGAAA   180

AGAGCATGCA CCTCGGCCGC CTTCCCTCTC GCCCACCTCT ACCCGGCAGC GGGGGCAGTC   240

AGAGCGGASC AAG ATG CGA ATG GGC CCT GGA AGA AAG CGG GAC TTT TCC   289
           Met Arg Met Gly Pro Gly Arg Lys Arg Asp Phe Ser
               -60   -55   -50

CCT GTT CCT TGG AGT CAG TAT TTT GAG TCC ATG GAA GAT GTA GAA GTA   337
Pro Val Pro Trp Ser Gln Tyr Phe Glu Ser Met Glu Asp Val Glu Val
            -45   -40   -35

GAG AAT GAA ACT GGC AAG GAT ACT TTT CGA GTC TAC AAG AGT GGT TCA   385
Glu Asn Glu Thr Gly Lys Asp Thr Phe Arg Val Tyr Lys Ser Gly Ser
            -30   -25   -20

GAG GGT CCA GTC CTG CTC CTT CTG CAT GGA GGA GGT CAT TCT GCC CTT   433
Glu Gly Pro Val Leu Leu Leu Leu His Gly Gly Gly His Ser Ala Leu
            -15   -10   -5

TCT TGG GCT GTG TTC ACG GCA GCT ARG   460
Ser Trp Ala Val Phe Thr Ala Ala Xaa
 1   5

(2) INFORMATION FOR SEQ ID NO: 121:

       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 275 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 207..245
             (C) IDENTIFICATION METHOD: Von Heijne matrix

```
          (D) OTHER INFORMATION:  score 4.6
                                  seq MIFLLYLLPSSEE/RR

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:


AAACAGACAG GTATGGAGTC TGGGTGGGGC CACGTGTACC CTCCCATCCT TAGAAAGAGT    60

GTGACACCAA GGGACAGATG CTGGCGTASG CGGGTTTTGT TTTGGAGGGT TTTTTGTTTG   120

TTTTTACAAA AATTAAGATA TTTCTGAGTT TATTATGAGG CTTTTAGTTT TACAATCATA   180

CTAAAAGATA ATTGTTCCTC TATAAA ATG ATT TTC CTT CTG TAC CTC TTG CCT    233
                             Met Ile Phe Leu Leu Tyr Leu Leu Pro
                                     -10                     -5

TCT TCT GAA GAA AGG AGA AAA TTG CTT TTT AGT CCC CAC AGG             275
Ser Ser Glu Glu Arg Arg Lys Leu Leu Phe Ser Pro His Arg
          1           5               10
```

(2) INFORMATION FOR SEQ ID NO: 122:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 445 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

     (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 236..418
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 4.6
                              seq LLLLHGGGHSALS/WA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
GCGGTAGGCG GGTGCTACGG GTAGCTGGGT GCTGTCCAAA GGCGACAGGG CGTCGTTAGG    60

GGAGCGAGTC GTGACCGGTT GGGCCACACT CAACGTGGGA CGAAGCTTCG CCTACTGTTT   120

GACTACGTGC GTGCAGCCTC CCCTCGATGT CGGCCCTCGA AAAGAGCATG CACCTCGGCC   180

GCCTTCCCTC TCGCCCACCT CTACCCGGCA GCGGGGGCAG TCAGAGCGGA SCAAG ATG    238
                                                              Met

CGA ATG GGC CCT GGA AGA AAG CGG GAC TTT TCC CCT GTT CCT TGG AGT    286
Arg Met Gly Pro Gly Arg Lys Arg Asp Phe Ser Pro Val Pro Trp Ser
-60                 -55                 -50                 -45

CAG TAT TTT GAG TCC ATG GAA GAT GTA GAA GTA GAG AAT GAA ACT GGC    334
Gln Tyr Phe Glu Ser Met Glu Asp Val Glu Val Glu Asn Glu Thr Gly
```

```
                    -40                        -35                        -30
AAG GAT ACT TTT CGA GTC TAC AAG AGT GGT TCA GAG GGT CCA GTC CTG        382
Lys Asp Thr Phe Arg Val Tyr Lys Ser Gly Ser Glu Gly Pro Val Leu
            -25                        -20                    -15

CTC CTT CTG CAT GGA GGA GGT CAT TCT GCC CTT TCT TGG GCT GTG TTC        430
Leu Leu Leu His Gly Gly Gly His Ser Ala Leu Ser Trp Ala Val Phe
            -10                        -5                     1

ACG GCA GCG ACA TGG                                                    445
Thr Ala Ala Thr Trp
  5
```

(2) INFORMATION FOR SEQ ID NO: 123:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 138 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 49..96
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.5
                           seq LLNLISILASIPS/QF

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
ATATACTGAA TTAAGTGTCT CTTGGTAATA CAGGCTCTTA TCAAACCC ATG CTG AGC        57
                                                      Met Leu Ser
                                                      -15

CTA TTA AAT CTC ATT TCA ATC TTA GCA AGT ATT CCC AGT CAA TTT AAA       105
Leu Leu Asn Leu Ile Ser Ile Leu Ala Ser Ile Pro Ser Gln Phe Lys
            -10                    -5                     1

CCA CAG TTT AGC AAG CTG CCA CTC TCA GGC CGG                           138
Pro Gln Phe Ser Lys Leu Pro Leu Ser Gly Arg
  5                    10
```

(2) INFORMATION FOR SEQ ID NO: 124:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 94 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 11..85
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 4.5
                   seq LMLLWPVHPLLVG/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:


```
AAGATTCATC ATG GGC ACC ACC TCC AAC ATG GTC ACC ACC ATC CAT CTC        49
           Met Gly Thr Thr Ser Asn Met Val Thr Thr Ile His Leu
            -25             -20                 -15

ATG TTG CTG TGG CCA GTG CAT CCA TTA CTG GTG GGC CAC CGC GGG           94
Met Leu Leu Trp Pro Val His Pro Leu Leu Val Gly His Arg Gly
  -10             -5                  1
```


(2) INFORMATION FOR SEQ ID NO: 125:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 481 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 41..343
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.4
                   seq ISHILAFFAASDG/IV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:


```
AAGTTCCCTC AGCGCCCGTA GCTTCGGCGG AGTCTGCGCG ATG GGC GAC CCG GAA       55
                                            Met Gly Asp Pro Glu
                                             -100

AGG CCG GAA GCG GCC GGG CTG GAT CAG GAT GAG AGA TCA TCT TCA GAC      103
Arg Pro Glu Ala Ala Gly Leu Asp Gln Asp Glu Arg Ser Ser Ser Asp
 -95             -90                 -85

ACC AAC GAA AGT GAA ATA AAG TCA AAT GAA GAG CCA CTC CTA AGA AAG      151
Thr Asn Glu Ser Glu Ile Lys Ser Asn Glu Glu Pro Leu Leu Arg Lys
```

```
-80                    -75                    -70                    -65

AGT TCT CGC CGG TTT GTC ATC TTT CCA ATC CAG TAC CCT GAT ATT TGG      199
Ser Ser Arg Arg Phe Val Ile Phe Pro Ile Gln Tyr Pro Asp Ile Trp
                -60                 -55                 -50

AAA ATG TAT AAA CAG GCA CAG GCT TCC TTC TGG ACA GCA GAA GAG GTC      247
Lys Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp Thr Ala Glu Glu Val
                -45                 -40                 -35

GAC TTA TCA AAG GAT CTC CCT CAC TGG AAC AAG CTT AAA GCA GAT GAG      295
Asp Leu Ser Lys Asp Leu Pro His Trp Asn Lys Leu Lys Ala Asp Glu
                -30                 -25                 -20

AAG TAC TTC ATC TCT CAC ATC TTA GCC TTT TTT GCA GCC AGT GAT GGA      343
Lys Tyr Phe Ile Ser His Ile Leu Ala Phe Phe Ala Ala Ser Asp Gly
                -15                 -10                 -5

ATT GTA AAT GAA AAT TTG GTG GAG CGC TTT AGT CAG GAG GTG CAG GTT      391
Ile Val Asn Glu Asn Leu Val Glu Arg Phe Ser Gln Glu Val Gln Val
 1               5                  10                  15

CCA GAG GCT CGC TGT TTC TAT GGC TTT CAA ATT CTC ATC GAG AAT GTT      439
Pro Glu Ala Arg Cys Phe Tyr Gly Phe Gln Ile Leu Ile Glu Asn Val
            20                  25                  30

CAC TCA GAG ATG TAC AGT TTG CTG ATA GAC ACT TAC ATC AGA             481
His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr Tyr Ile Arg
            35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO: 126:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 197 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 3..50
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.4
                                    seq GLFSLLPHPPCVG/RV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
AG ATG GAT GCA GGC TTA TTT TCT CTG CTT CCC CAT CCT CCA TGT GTT       47
   Met Asp Ala Gly Leu Phe Ser Leu Leu Pro His Pro Pro Cys Val
       -15                 -10                 -5

GGC AGG GTG CTG CCA CAG TCT AGG TAT CAT CTG CAT CCA AGA TCA CCT      95
```

```
Gly Arg Val Leu Pro Gln Ser Arg Tyr His Leu His Pro Arg Ser Pro
 1               5               10                  15

TTG GTA GAA GAT ACC TGT TTC TTC CAG AGG CTT AAA AAA ATT TTA AAT   143
Leu Val Glu Asp Thr Cys Phe Phe Gln Arg Leu Lys Lys Ile Leu Asn
             20              25              30

AAA ATA GGA AAC CTT TTC CAT TCA ACA AAG TCC CTT TGT GTC TCA CTT   191
Lys Ile Gly Asn Leu Phe His Ser Thr Lys Ser Leu Cys Val Ser Leu
         35              40              45

GCC CCG                                                           197
Ala Pro
```

(2) INFORMATION FOR SEQ ID NO: 127:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 121 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 65..106
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.4
                                    seq LITLTYLIQGESA/RT

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
ATTTAATAAC TTAAAAATTG GCCAATTTTA TTTTTAGAAA AGCTCTGCAT CATCCTGTGT   60

TTAG ATG TTA ATT ACG CTG ACT TAC CTA ATC CAG GGT GAG TCA GCA CGA   109
     Met Leu Ile Thr Leu Thr Tyr Leu Ile Gln Gly Glu Ser Ala Arg
              -10             -5                  1

ACC ACG TTC GAG                                                     121
Thr Thr Phe Glu
 5
```

(2) INFORMATION FOR SEQ ID NO: 128:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 238 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 146..223
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.4
                                  seq RVQCLCAIPFAFS/LT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

AAAATATGTC TTCAGCTCTA ATCCATTATC ACTCAGATCA TTCTAACCTT TTCCCCTTGC   60

TTATCTATAA CTTTCCACTT CAACAGTGAG AAACCTGGCT TCCATATCTG TCATCCATAA   120

ATGTACGTAT TTAATTCCAG TACAC ATG TAT ACT GGT TTC AGA ATA GAA GCA   172
                            Met Tyr Thr Gly Phe Arg Ile Glu Ala
                            -25   -20

ACT TTA TTA ACT AGA GTG CAG TGC TTA TGT GCA ATT CCT TTT GCC TTT   220
Thr Leu Leu Thr Arg Val Gln Cys Leu Cys Ala Ile Pro Phe Ala Phe
    -15   -10   -5

AGT CTT ACA GGC ATC CGG   238
Ser Leu Thr Gly Ile Arg
    1   5

(2) INFORMATION FOR SEQ ID NO: 129:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 419 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 252..392
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.4
                                  seq ISHILAFFAASDG/IV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

AAGCGGACCA CCTGGGTGCT GTCGTAGTTG GAGGTGGCCT GAGGAGCTCA GTTCCCTCAG   60

CGCCCGTAGT TTCGGCGGAG TCTGCGCGAT GGGCGACCCG GAAAGGCCGG GAAGCGGCCG   120

GGCTGGATCA GGATGAGAGA TCATCTTCAG ACACCAACGA AAGTGAAATA AAGTCAAATG   180

AAGAGCCRST CCTAAGAAAG AGTTCTCGCC GGTTTGTCAT CTTTCCAATC CAGTACCCTG   240

```
ATATTTGGAA A ATG TAT AAA CAG GCA CAG GCT TCC TTC TGG ACA GCA GAA    290
           Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp Thr Ala Glu
           -45             -40                         -35
```

```
GAG GTC GAC TTA TCA AAG GAT CTC CCT CAC TGG AAC AAG CTT AAA GCA    338
Glu Val Asp Leu Ser Lys Asp Leu Pro His Trp Asn Lys Leu Lys Ala
            -30             -25                     -20
```

```
GAT GAG AAG TAC TTC ATC TCT CAC ATC TTA GCC TTT TTT GCA GCC AGT    386
Asp Glu Lys Tyr Phe Ile Ser His Ile Leu Ala Phe Phe Ala Ala Ser
            -15             -10                 -5
```

```
GAT GGA ATT GTA AAT GAA AAT TTG GTG GAG CGC                         419
Asp Gly Ile Val Asn Glu Asn Leu Val Glu Arg
        1           5
```

(2) INFORMATION FOR SEQ ID NO: 130:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 255 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 112..195
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.3
                              seq FLGLAAMASPSRN/SQ

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AATTACGATG TKKTGTGTGC TTGTGCAAAT ACAGGACGGT TCCTGAAATG TGTCTCTGAG   60

```
CGTTCTTAAC TGTGTGTRAG GAATTSMTGC GCGTACACGT GGTGGGTCAT T ATG CTG    117
                                                       Met Leu
```

```
CTG CAC CTG TGT AGT GTG AAG AAT CTG TAC CAG AAC AGG TTT TTA GGC    165
Leu His Leu Cys Ser Val Lys Asn Leu Tyr Gln Asn Arg Phe Leu Gly
    -25             -20                 -15
```

```
CTG GCC GCC ATG GCG TCT CCT TCT AGA AAC TCC CAG AGC CGA CGC CGG    213
Leu Ala Ala Met Ala Ser Pro Ser Arg Asn Ser Gln Ser Arg Arg Arg
-10             -5                  1               5
```

```
TGC AAG GAG CCG CTC CGA TAC AGC TAC AAC CCC GAC CAG GGG            255
Cys Lys Glu Pro Leu Arg Tyr Ser Tyr Asn Pro Asp Gln Gly
```

(2) INFORMATION FOR SEQ ID NO: 131:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 287 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 123..176
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.3
                              seq WTCLKSFPSPTSS/HA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AAGAGCATCC TGCGCCCCGG CGCGGGGCCC TGCGGTAGCC TCAGGCCCCT CCCCTGGACC   60

CGCCGCAGAG CCAGTGCAGA ATACAGAAAC TGCAGCCATG ACCACGCACG TCACCCTGGA   120

AG ATG CCC TGT CCA ACG TGG ACC TGC TTG AAG AGC TTC CCC TCC CCG   167
   Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
        -15   -10   -5

ACC AGC AGC CAT GCA TCG AGC CTC CAC CTT CCT CCA TCA TGT ACC AGG   215
Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
              1   5   10

CTA ACT TTG ACA CAA ACT TTG AGG ACA GGA ATG CAT TTG TCA CGG GCA   263
Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
      15   20   25

TTG CAA GGT ACA TTG ACC AGG CAG   287
Leu Gln Gly Thr Leu Thr Arg Gln
  30   35

(2) INFORMATION FOR SEQ ID NO: 132:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 224 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:

.(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 6..104
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 4.3
                    . seq LLGWGLNLTLGQG/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:


```
AAAGG ATG GAG GAT CTC TTT AGC CCC TCA ATT AWG CCG CCG GCG CCC AAC   50
      Met Glu Asp Leu Phe Ser Pro Ser Ile Xaa Pro Pro Ala Pro Asn
          -30             -25                 -20

ATT TCC GTG CCC ATC TTG CTG GGC TGG GGT CTC AAC CTG ACC TTG GGG     98
Ile Ser Val Pro Ile Leu Leu Gly Trp Gly Leu Asn Leu Thr Leu Gly
        -15             -10                 -5

CAA GGA GCC CCT GCC TCT GGG CCG CCC AGC CGC CGC GTC CGC CTG GTG    146
Gln Gly Ala Pro Ala Ser Gly Pro Pro Ser Arg Arg Val Arg Leu Val
        1           5           10

TTC CTG GGG GTC ATC CTG GTG GTG GCG GTG GCA KGC AAC ACC ACA GTG    194
Phe Leu Gly Val Ile Leu Val Val Ala Val Ala Xaa Asn Thr Thr Val
15          20          25          30

CTG TGC CGC CTG TGC GGC GGC GGC GGG CCG                            224
Leu Cys Arg Leu Cys Gly Gly Gly Gly Pro
            35          40
```


(2) INFORMATION FOR SEQ ID NO: 133:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 347 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 183..338
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                    seq VMLETCGLLVSLG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:


```
AGGGACTTCC GGCCTCGCTG GCGTGGACGT TTGTGGTGGG GCGTGTTGGT CCGCGCTCTC   60
```

AGAACTGTGC TGGGAAGGAT GGTAGGGCGA CTGGGGCTCA CCTCCGCACC GTTGTAGGAC   120

CCGGGGTAGG GTTTTGAGCC CGTGGGAGCK GCCCCACGCG GCCTCGTCCT GCCAACGGTC   180

```
GG ATG GCG GAG ACG AAG GAC GCA GCG CAG ATG TTG GTG ACC TTC AAG       227
   Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
       -50               -45               -40

GAT GTG GCT GTG ACC TTT ACC CGG GAG GAG TGG AGA CAG CTG GAC CTG      275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
        -35               -30               -25

GCC CAG AGG ACC CTG TAC CGA GAG GTG ATG CTG GAG ACC TGT GGG CTT     323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
        -20               -15               -10

CTG GTT TCA CTA GGG CAT CCT CGG                                      347
Leu Val Ser Leu Gly His Pro Arg
 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 134:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 432 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: DOUBLE
    (D) TOPOLOGY: LINEAR

  (ii) MOLECULE TYPE: CDNA

  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

  (ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 298..336
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 4.1
           seq MLILSQNIAQLEA/QV

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

AATTGARRTG TTTGATAACT GTCACTTTAG GGTTTCAACC AAAACCTTGA CTTTATCATC   60

TTGTTATACA TTTTTCAAAA TGAGGTTAGA GATCAGGGGA ATGAATAGGA GAGAAGTACA   120

TATTTCAGTT CACTGGGCAT AGGTGAATAG AGGAAGGAGA AAATGAACAT ACCCAATCCA   180

CAGAGAAATG GCTCACAGAG CCCAGTGACT ATGCTGAGAC GCTATTAATT CAAGAAAGTT   240

TTAGTATTTG ATTTGTCAAA TGACATTATT GTTTAGGACT TTTATTTTCC CTTACAG   297

```
ATG TTG ATC TTG TCT CAG AAT ATT GCC CAA CTG GAG GCC CAG GTG GAA      345
Met Leu Ile Leu Ser Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu
        -10               -5                1

AAG GTT ACA AAG GAA AAG ATT TCA GCT ATT AAT CAA CTG GAG GAA AAT      393
```

```
Lys Val Thr Lys Glu Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Asn
  5               10              15
```

```
TCA AAG CCA GCT GGC TTC TCG GGA AAA TGG ATG TCA CAA              432
Ser Lys Pro Ala Gly Phe Ser Gly Lys Trp Met Ser Gln
 20          ·      25              30
```

(2) INFORMATION FOR SEQ ID NO: 135:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 380 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 90..152
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                              seq GLWAHSWTCSCSA/AX

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```
AATTCACTTC ACCTGGAGTT GAGCCAAGAT TCTCTTTACT CCAAAGCCAG CACTCCTTCT   60
```

```
GAGAACAGGA CTTTGATTTG GATGGACGG ATG TTG CTG GGG GCC TCA GCA CAG    113
                            Met Leu Leu Gly Ala Ser Ala Gln
                                -20              -15
```

```
GGT CTT TGG GCT CAC AGC TGG ACA TGC AGC TGT TCA GCG GCA STG CGG    161
Gly Leu Trp Ala His Ser Trp Thr Cys Ser Cys Ser Ala Ala Xaa Arg
        -10              -5                      1
```

```
TCT GTC CAC CCA GGC GGA GAC TGG ATG CAA CAG TTT CAG GCG GGG TTC    209
Ser Val His Pro Gly Gly Asp Trp Met Gln Gln Phe Gln Ala Gly Phe
    5               10              15
```

```
CTC CCT CCC CAG GTG CCT GCC CAC CTC TCC CTT ACA TGG GAT GTC TCT    257
Leu Pro Pro Gln Val Pro Ala His Leu Ser Leu Thr Trp Asp Val Ser
 20              25              30              35
```

```
CTT CTT CCT CCT TGC CTG GTC CCT AAA GCA CTT GAG TTT GTG GTT CAT    305
Leu Leu Pro Pro Cys Leu Val Pro Lys Ala Leu Glu Phe Val Val His
             40              45              50
```

```
TTT TTA AAA AAT GAT ATA TTT TAT TTA ACC CAG TAT ATT AAA AAT GTC    353
Phe Leu Lys Asn Asp Ile Phe Tyr Leu Thr Gln Tyr Ile Lys Asn Val
             55              60              65
```

```
ATT TCA GAA TGT ACG TTT TCC TTT TTT                                380
Ile Ser Glu Cys Thr Phe Ser Phe Phe
```

70   75

(2) INFORMATION FOR SEQ ID NO: 136:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 212 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 9..53
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                                seq APLELSCWGGGWG/LP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGCGCAAG ATG GCG GCC CCC TTG GAA CTC AGT TGC TGG GGA GGC GGC TGG   50
         Met Ala Ala Pro Leu Glu Leu Ser Cys Trp Gly Gly Gly Trp
         -15   -10   -5

GGA CTC CCA TCG GTT CAC AGC GAG TCC CTG GTG GTG ATG GCT TAT GCC   98
Gly Leu Pro Ser Val His Ser Glu Ser Leu Val Val Met Ala Tyr Ala
 1   5   10   15

AAA TTT TCT GGT GCA CCC TTG AAA GTC AAT GTG ATA GAT AAC ACC TGG   146
Lys Phe Ser Gly Ala Pro Leu Lys Val Asn Val Ile Asp Asn Thr Trp
             20   25   30

AGA GGT TCA AGA GGC GAT GTA CCA ATT TTG ACA ACT GAA GAC GAC ATG   194
Arg Gly Ser Arg Gly Asp Val Pro Ile Leu Thr Thr Glu Asp Asp Met
             35   40   45

GTT TCT CAG CCA GCA AGG   212
Val Ser Gln Pro Ala Arg
         50

(2) INFORMATION FOR SEQ ID NO: 137:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 432 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:

.(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 226..285
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq LGFLNCYIAVARS/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

AAGGGAMNSA CCCAGGCTGC GGGACSGGTG CAGGCTGCGG CGCTGACGGC CTCTGCTCCT   60

TCCGCGGGTT TCCGACTCCC TGCCCTAGAT TTTCTGCTTA GCGACTTGGG GTCCCCTCTC   120

GTTTGCTTCT GGTAGGAGTC GCAATCCCAK BAGCAATAGC CCAGAAGAGG ACACGGTTCC   180

CGTACCGAAG GTTCAGTACC AGCAGCCCGA CCATCACGCG GCGGG ATG TCT GDR GTT   237
                                                Met Ser Xaa Val
                                                -20

GGC ATT GAC CTC GGC TTT CTC AAC TGC TAC ATT GCT GTC GCG AGA AGT   285
Gly Ile Asp Leu Gly Phe Leu Asn Cys Tyr Ile Ala Val Ala Arg Ser
   -15   -10   -5

GGC GGC ATC GAG ACC ATC GCC AAT GAG TAC AGC GAC AGG TGT ACC CCG   333
Gly Gly Ile Glu Thr Ile Ala Asn Glu Tyr Ser Asp Arg Cys Thr Pro
 1   5   10   15

GCC TGT ATA TCA TTG GGA TCA AGA ACT CGA GCC ATT GGA AAT GCA GCA   381
Ala Cys Ile Ser Leu Gly Ser Arg Thr Arg Ala Ile Gly Asn Ala Ala
            20   25   30

AAG AGC CAG ATA GTC ACG AAC GTA AGA AAT ACA ATT CAT GGC TTC AAA   429
Lys Ser Gln Ile Val Thr Asn Val Arg Asn Thr Ile His Gly Phe Lys
         35   40   45

AAG   432
Lys

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 101..157

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
                                 seq FVVFSTMFTASSP/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

AGATGAATAT TTGATACCCA CAGTAGAACT TCTTTMMGAA CTTCTTTCAC AATWGGAGTT   60

AATCTTCTAA AGCCCCGCCA CTGCTTCATC AACTAAGTTT ATG GAA TAT TCT AAA   115
                                             Met Glu Tyr Ser Lys
                                                             -15

TMM TTT GTT GTC TTT TCA ACA ATG TTC ACA GCA TCT TCA CCA GGA GAA   163
Xaa Phe Val Val Phe Ser Thr Met Phe Thr Ala Ser Ser Pro Gly Glu
        -10   -5   1

GAC TTT CCC CCC TTC TTT TCA CAG ATG TNS AGA TTG TCA AGA AAC TAC   211
Asp Phe Pro Pro Phe Phe Ser Gln Met Xaa Arg Leu Ser Arg Asn Tyr
        5   10   15

TTT CCT TGC CCA CCR WGG   229
Phe Pro Cys Pro Pro Xaa
    20

(2) INFORMATION FOR SEQ ID NO: 139:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 328 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 113..232
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.1
                                     seq LPFRLPWASTATA/RC

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AACACCCAGG CCCTGATGCA GCAGCAGGCG GCCCTGGTAG CGGCTCACAG TGCCTACCTC   60

AGCCCCATGG CCACCATGGC TGCCGTGCAG ATGCAGCACA TGGCTGCCAT CA ATG CCA   118
                                                           Met Pro
                                                            -40

ATG GCC TCA TCG CCA CCC CCA TCA CCC CAT CCT CAG GAA CCA GCA CCC   166
Met Ala Ser Ser Pro Pro Pro Ser Pro His Pro Gln Glu Pro Ala Pro
        -35   -30   -25

```
CTC CTG CCA TCG CTG CCA CGC CTG TCT CTG CCA TTC CGG CTG CCC TGG      214
Leu Leu Pro Ser Leu Pro Arg Leu Ser Leu Pro Phe Arg Leu Pro Trp
        -20             -15             -10

GCG TCA ACG GCT ACA GCC CGG TGC CCA CCC AGC CCA CTG GGC AGC CTG      262
Ala Ser Thr Ala Thr Ala Arg Cys Pro Pro Ser Pro Leu Gly Ser Leu
    -5               1               5               10

CNC CTG ATG CTC TGT ATC CCA ACG GGG TTC ACC CCT ACC CAG CCC AGA      310
Xaa Leu Met Leu Cys Ile Pro Thr Gly Phe Thr Pro Thr Gln Pro Arg
            15              20              25

GCC CCG CGG CCC CCT GGG                                              328
Ala Pro Arg Pro Pro Gly
        30
```

(2) INFORMATION FOR SEQ ID NO: 140:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 217 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 53..166
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4
                         seq WALGLKFLSSSSQ/NF

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```
AACAGGAGAC TTGGGAAGGA CCAATGGTAA TTTAAGTGGC TCTTAAAAAG TC ATG CAA    58
                                                           Met Gln

CAT GTW WCT GGA CAC GWW CCT GAT CCT ATT GCG ATA ATG TAT GTG TGC     106
His Val Xaa Gly His Xaa Pro Asp Pro Ile Ala Ile Met Tyr Val Cys
        -35             -30              -25

CCT CCC TGT GGG CAC ACC ACC TGG GCA TTA GGA CTG AAA TTC CTG AGT     154
Pro Pro Cys Gly His Thr Thr Trp Ala Leu Gly Leu Lys Phe Leu Ser
-20              -15             -10                   -5

TCT TCC TCT CAA AAT TTC TGT GCA CCA GTA TTA TTC CTC ATT TTA CAT     202
Ser Ser Ser Gln Asn Phe Cys Ala Pro Val Leu Phe Leu Ile Leu His
             1               5               10

ACA GGA GGC CAA CGG                                                 217
Thr Gly Gly Gln Arg
        15
```

(2) INFORMATION FOR SEQ ID NO: 141:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 202 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 44..133
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 4
                                       seq AGFLKCLLLSSLQ/SY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

ATAATAGTGT TATTTCAGTG CATGATTTTT GCCTTTGAGA GAC ATG GGT TGG GAA   55
                                                 Met Gly Trp Glu
                                                 -30

ATG ACA TGT ATT AAG TCT TTT TTC TGG GCC AGG TCT CAT GCT GGG TTC   103
Met Thr Cys Ile Lys Ser Phe Phe Trp Ala Arg Ser His Ala Gly Phe
    -25   -20   -15

TTG AAA TGC CTC CTG TTG TCT TCA TTA CAG TCC TAC AAG GAG GCT GCT   151
Leu Lys Cys Leu Leu Leu Ser Ser Leu Gln Ser Tyr Lys Glu Ala Ala
-10   -5   1   5

GTT ATC TTC CCT CTT ACT GAT TTG CTC AAA CTG AAA GAT TAT GGT GAA   199
Val Ile Phe Pro Leu Thr Asp Leu Leu Lys Leu Lys Asp Tyr Gly Glu
            10   15   20

TGG   202
Trp

(2) INFORMATION FOR SEQ ID NO: 142:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 361 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

```
       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 248..355
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:   score 4
                                   seq VQLSFAATTPVLA/DK

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:


AAGTTGGGAG AGGAGCTGCT GGTTGAAGTG AAGGTGAGGA GCTCAGTGCT TCTTTCACTG    60

CCCTATCTGC TGGGCTTTAC GCCCCTGAGG GGCTGACTGT AAAAAACTCT AAGCTGATCC   120

AGCCCCCAAA ATTCACCTTT GGTGAGCTGG AAAGTCCATC TATTTGGGAC GCGAATCATG   180

TCAGTGCGAC AACGCAAAAG GGTTGAAAGC CTTCTACGAT GCAATAAAAT ACGGGCCTAA   240

CCACTTG ATG GTG TTT GGA GGC GTC TGT CCA TCC GTC ACA TCC ATC ATT    289
        Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile
        -35                 -30                 -25

GCA GAG TCC CTC CAA GGC TGG AAT CTG GTG CAG CTT TCT TTT GCT GCA    337
Ala Glu Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala
    -20                 -15                 -10

ACC ACG CCT GTT CTA GCC GAT AAG                                    361
Thr Thr Pro Val Leu Ala Asp Lys
    -5                  1



(2) INFORMATION FOR SEQ ID NO: 143:

         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 216 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 145..192
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:   score 4
                                    seq ITWSLLFLYQCSL/HF

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:


ACACATTACC TCTTTTCATT TTAGACAGGT TAATTAGTGT GTATTTCCAT AGTTGTCTTT    60

TACCTCAAGA AATAATCATT TCTTTAGGTA ATTATTTTAA TGGCTTGCCA TTTTGTATGA   120

TTGTTCTTGC AAACATTTCT ATTT ATG CAT TTT ATA ACA TGG AGC TTA CTA     171
```

```
                      Met His Phe Ile Thr Trp Ser Leu Leu
                          -15                   -10


TTT TTA TAC CAG TGC TCG CTT CAT TTT ATC ATT ATC AAG GCC GGG        216
Phe Leu Tyr Gln Cys Ser Leu His Phe Ile Ile Ile Lys Ala Gly
        -5                   1                 5
```

(2) INFORMATION FOR SEQ ID NO: 144:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 378 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 256..363
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                        seq CWPSVASPSSSWS/SP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
AAAGTGGCCA GCGGACCATC TCTCGTGCCC TCGCTCTCTG CGCTCCGGGG CAGCTGAGCC    60

CCGGCCACCC GCTCTCCAAG ATGAAGAAGC TCCAGGGAGC TCACCTCCGC AAGCCTGTCA   120

CCCCAGACCT GCTGATGACC CCCAGTGACC AGGGCGATGT CGACCTGGAT GTGGACTTTG   180

CTGCACACCG GGGGAACTGG ACAGGCAAGC TGGACTTCCT GCTGTCCTGC ATTGGCTACT   240

GTGTAGGCCT GGGGA ATG TCT GGC GCT TCC CCT ATC GAG CGT ACA CCA ATG    291
                Met Ser Gly Ala Ser Pro Ile Glu Arg Thr Pro Met
                -35                   -30                     -25

GAG GAG GCG CCT TCC TCG TGC CCT ACT TCC TCA TGC TGG CCA TCT GTG    339
Glu Glu Ala Pro Ser Ser Cys Pro Thr Ser Ser Cys Trp Pro Ser Val
            -20                   -15                 -10

GCA TCC CCC TCT TCT TCC TGG AGC TCT CCC TGG GCC AGT              378
Ala Ser Pro Ser Ser Ser Trp Ser Ser Pro Trp Ala Ser
            -5                   1                 5
```

(2) INFORMATION FOR SEQ ID NO: 145:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE

                    (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 172..282
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 3.9
                                      seq PGPSLRLFSGSQA/SV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

AAGGGTCTCC ATGACAACCG GCCTGGCCGG CTAGCAGTGC TCTGCTCACT TGGCTGCGAG   60

GAGCGCCACG AAAGGTCAGA GGAAGGAGCT GTGGGAAGCT CGCAGCAGGT ATCGGAGCTT   120

AAGCCAGTGG ATTTGGGGGC CCTGGGCTCC CTAGCCGGCT GCGGTGTGAG A ATG GAG   177
                                                           Met Glu

TGG GCA GGA AAG CAG CGG GAC TTT CAG GTA AGG GCA GCT CCG GGC TGG   225
Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro Gly Trp
-35   -30   -25   -20

GAT CAT TTG GCC TCC TTT CCT GGC CCT TCT CTC CGG CTG TTT TCT GGG   273
Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe Ser Gly
                -15   -10   -5

AGT CAG GCG AGT GTC TGT AGT CTC TGC TCG GGG TTT GGG GCT CAG GAA   321
Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala Gln Glu
                 1   5   10

(2) INFORMATION FOR SEQ ID NO: 146:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 278 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 78..257
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 3.9
                                      seq AKVVSLSLQTSSA/HH

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

AAGAACACAA AAAGCTACAG AAGGTCCAGG CTACTGAAAA GCATCAAGAC CAAGCTGTTG   60

TAAGTCAAAC TGCTTTT ATG ATT GCA TTC TTT GAT GAA GAC AAT CCC AGA   110
                Met Ile Ala Phe Phe Asp Glu Asp Asn Pro Arg
                -60   -55   -50

AAA AGA AGG TCG TAT TCT TTT ACT CAA AGT GCG GGA ATC TTG TGT CAG   158
Lys Arg Arg Ser Tyr Ser Phe Thr Gln Ser Ala Gly Ile Leu Cys Gln
            -45   -40   -35

GAA ACT ACA TAT TCA ACA CCA CAT ACA AAA CTT GAG AAA GCA AAG TCT   206
Glu Thr Thr Tyr Ser Thr Pro His Thr Lys Leu Glu Lys Ala Lys Ser
            -30   -25   -20

CCA ACA GCA GAT GCC AAA GTG GTT TCT TTG TCT TTA CAG ACT AGC TCT   254
Pro Thr Ala Asp Ala Lys Val Val Ser Leu Ser Leu Gln Thr Ser Ser
            -15   -10   -5

GCG CAT CAC AGA GGG GGG MDT GGT   278
Ala His His Arg Gly Gly Xaa Gly
    1   5

(2) INFORMATION FOR SEQ ID NO: 147:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 349 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 89..232
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.9
                                    seq ALFCTLPCPVERG/QQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AAATTTTCTT AAATTAGCAG TCTAATGTGT TCTAAAGAGC AGCTCCACTC AGATCTCTTC   60

TTAAGGGTTG CATTTCATCA CAGTATAA ATG GGC AAA TCC ATC AYT TCC CTC   112
                               Met Gly Lys Ser Ile Xaa Ser Leu
                                               -45

TGC TCA GTG CKC TTG AAR GCG AGA TTG AAG GGM MAA TTA GAA GCT GTT   160
Cys Ser Val Xaa Leu Lys Ala Arg Leu Lys Gly Xaa Leu Glu Ala Val
-40   -35   -30   -25

CAT TTG TGC TTG CGG GCT CAG AAG CGT CGC ACT GCT TTG TTT TGT ACT   208

```
His Leu Cys Leu Arg Ala Gln Lys Arg Arg Thr Ala Leu Phe Cys Thr
            -20              -15               -10

CTA CCG TGT CCT GTT GAA AGG GGT CAA CAA GTG CCG GGG ANV NNN AHG    256
Leu Pro Cys Pro Val Glu Arg Gly Gln Gln Val Pro Gly Xaa Xaa Xaa
        -5                   1               5

AGG CTG AGG CTG GCG TCA CCT TCC GTT GCT AAG GTG TTC CAG TGT TTT    304
Arg Leu Arg Leu Ala Ser Pro Ser Val Ala Lys Val Phe Gln Cys Phe
    10               15               20

CTC TCA AAA CTC TGT GTT TGG AAC ATC AAG GAT GGA TTA TCC CGG        349
Leu Ser Lys Leu Cys Val Trp Asn Ile Lys Asp Gly Leu Ser Arg
25               30               35
```

(2) INFORMATION FOR SEQ ID NO: 148:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 210 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 52..96
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.9
                                    seq LHMTLFRVPFTFS/XF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
ACACAAAGGA AAATGGCAGG GATATGAATT TCTTTCCCAG CTTTTATATA G ATG TGC    57
                                                          Met Cys
                                                          -15

CTG CAT ATG ACA CTC TTT AGA GTT CCT TTC ACT TTT TCT KTT TTT TGG    105
Leu His Met Thr Leu Phe Arg Val Pro Phe Thr Phe Ser Xaa Phe Trp
        -10               -5               1

AAG GGG GCG GGG AGG CAG GAG GAG TGC AGT TTT AAG CCT AGC CTA TAC    153
Lys Gly Ala Gly Arg Gln Glu Glu Cys Ser Phe Lys Pro Ser Leu Tyr
5                10               15

TAC TAC AAA CTT ATT ATG GTA CTT AAA ATT GCA CTC CTC CTG TCC CCG    201
Tyr Tyr Lys Leu Ile Met Val Leu Lys Ile Ala Leu Leu Leu Ser Pro
20               25               30               35

CCC CCC AAG                                                        210
Pro Pro Lys
```

(2) INFORMATION FOR SEQ ID NO: 149:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 143 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 75..116
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                              seq LNILKTLTSAALP/SP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

AATACACCTT AAACTTTACT ACTTTTTATA AACGGTAGGA AAGGATATAC TGATGTTGTG   60

GGTATTACAA GGTA ATG CTG AAC ATT CTG AAG ACC TTA ACT TCT GCT GCT   110
             Met Leu Asn Ile Leu Lys Thr Leu Thr Ser Ala Ala
                       -10   -5

CTT CCC TCC CCC TCC CCC CGC CCC AAC AAG AGG   143
Leu Pro Ser Pro Ser Pro Arg Pro Asn Lys Arg
    1   5

(2) INFORMATION FOR SEQ ID NO: 150:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 176 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 24..143
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                              seq SPLLCLYHPPVYT/ST

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```
AGTAATCCCA GGCGTTCGCC CTC ATG CGG GCC AGG GTT TGG CCT CGC TCC CAC    53
                       Met Arg Ala Arg Val Trp Pro Arg Ser His
                       -40                 -35

GGG ATC CCT GTG CCT TCC TTT CTC TCT AAG AGC AGC CTC AGT CAT ACA     101
Gly Ile Pro Val Pro Ser Phe Leu Ser Lys Ser Ser Leu Ser His Thr
-30             -25             -20             -15

CCA TCA CCT CTC CTC TGT CTA TAC CAT CCT CCT GTC TAC ACC AGC ACC    149
Pro Ser Pro Leu Leu Cys Leu Tyr His Pro Pro Val Tyr Thr Ser Thr
                -10             -5              1

ACT ACC CCA TCT ATA CCA CCA CGT CTG                                 176
Thr Thr Pro Ser Ile Pro Pro Arg Leu
    5               10
```

(2) INFORMATION FOR SEQ ID NO: 151:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 414 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 262..369
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 3.9
                              seq SLCLSLLIPGPKP/LV

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
AAAGTAGGAA ATGGCTGCTT CACCCAGGAG GCACCAAGAT GCCCGTGTGT GGCTCTACTG    60

GTGATGCCCT GGTCTTCATT GAAAAGGCCA GCACCCGTTA CGTGGTCAGC ACAGACGTTG   120

CCGTGAATGA GGATTCCTTC CTACAGATAG ACTTCGCTGC CTCCTGCTCA GTCACAGACT   180

CTTGTTATGC GATTGAATTG GAATACTCAG TAGATCTTGG ATTGTCATGG CACCCATTGG   240

TAAGGGACTG TCTGCCTACC A ATG TGG AAT GCA GTC GCT ATC ATC TGC AAC    291
                       Met Trp Asn Ala Val Ala Ile Ile Cys Asn
                       -35                 -30

GGA TCC TGG TGT CAG ACA CDW TCA ACA AGT GGA CTA GAA TCA CTC TGC    339
Gly Ser Trp Cys Gln Thr Xaa Ser Thr Ser Gly Leu Glu Ser Leu Cys
    -25             -20             -15

CTC TCC CTC CTT ATA CCA GGT CCC AAG CCA CTC GTT TCC GTT GGC ATC    387
Leu Ser Leu Leu Ile Pro Gly Pro Lys Pro Leu Val Ser Val Gly Ile
-10             -5              1               5
```

```
AAC CAG CTC CTT TTG ACA AGC AGC AGA                          414
Asn Gln Leu Leu Leu Thr Ser Ser Arg
        10                  15
```

(2) INFORMATION FOR SEQ ID NO: 152:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 171 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 103..144
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                        seq LRLGLFKISWARC/LS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
AAAAATTATT TCTGCTTAAA CAACAGTTTC AAATATTTCT CTTTTGAAGA CAAAATTGGT    60

TTAGTTTCAG CAATGTATTG ATATAATTTT ACATTTTTTT AA ATG TTG AGG CTG      114
                                             Met Leu Arg Leu

GGT TTA TTT AAG ATT AGC TGG GCT CGC TGC CTA TCA TAT AGT AAA ACC    162
Gly Leu Phe Lys Ile Ser Trp Ala Arg Cys Leu Ser Tyr Ser Lys Thr
-10                 -5                  1                   5

CAG CBC GAA                                                        171
Gln Xaa Glu
```

(2) INFORMATION FOR SEQ ID NO: 153:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 262 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide

. (B) LOCATION: 80..187
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
                        seq VVEILPYLPCLTA/RD

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

AGGGGTACCG AGTCTCGTTT CCTCTCAGTC CATCCACCCT TCATGGGGCC AGAGCCCTCT   60

CTCCAGAATC TGAGCAGCA ATG CCG TTT GCT GAA GAC AAG ACC TAT AAG TAT   112
                     Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr
                     -35   -30

ATC TGC CGC AAT TTC AGC AAT TTT TGC AAT GTG GAT GTT GTA GAG ATT   160
Ile Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile
-25   .   -20   -15   -10

CTG CCT TAC CTG CCC TGC CTC ACA GCA AGA GAC CAG GAT CGA CTG CGG   208
Leu Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg
                -5   1   5

GCC ACC TGC ACA CTC TCA GGG AAC CGG GAC ACC CTC TGG CAT CTC TTC   256
Ala Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe
        10   15   20

AAT ACC   262
Asn Thr
    25

(2) INFORMATION FOR SEQ ID NO: 154:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 165 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 46..153
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.8
                                    seq GTDSLSFLPPCPC/CP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AATCATGAAA TCCTTGCAAC TCATTAAGTT TCCTGTTTGC TGTAG ATG CCA GGA AGC   57
                                              Met Pro Gly Ser
                                              -35

TCA GGG CTC AGA TTT ATA TGT AAG TCC AGG AAC CAT CCT CAG TTT GGG   105

```
Ser Gly Leu Arg Phe Ile Cys Lys Ser Arg Asn His Pro Gln Phe Gly
    -30                 -25                 -20

AGT TTC AGT GGA ACT GAC TCC CTT TCC TTC CTA CCA CCC TGC CCC TGT   153
Ser Phe Ser Gly Thr Asp Ser Leu Ser Phe Leu Pro Pro Cys Pro Cys
    -15                 -10                 -5

TGC CCG GCT GCG                                                    165
Cys Pro Ala Ala
  1
```

(2) INFORMATION FOR SEQ ID NO: 155:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 261 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 64..234
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.8
                          seq QLXLVMEFCGAGS/VT

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
ACATACGGGC AAGTTTATAA GGGTCGTCAT GTCAAAACGG GCCAGCTTGC AGCCATCAAG   60

GTT ATG GAT GTC ACA GGG GAT GAA GAG GAA GAA ATC AAA CAA GAA ATT   108
    Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile
        -55                 -50                 -45

AAC ATG TTG AAG AAA TAT TCT CAT CAC CGG AAT ATT GCT ACA TAC TAT   156
Asn Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr
    -40                 -35                 -30

GGT GCT TTT ATC AAA AAG AAC CCA CCA GGC ATG GAT GAC CAA CTT TGR   204
Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Xaa
    -25                 -20                 -15

TTG GTG ATG GAG TTT TGT GGT GCT GGC TCT GTC ACC GAC CTG ATC AAG   252
Leu Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys
-10                 -5                  1                   5

AAC ACA GGG                                                        261
Asn Thr Gly
```

(2) INFORMATION FOR SEQ ID NO: 156:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 126 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: CDNA

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 49..120
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:   score 3.8
                               seq KLFLVFLLNICKG/IV

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:
```

```
ATCTCTAGAA AGAAGAAGGC ATGCTACAAA TAGGAAGGAA TTGTAATA ATG ATA TTT    57
                                                      Met Ile Phe

GGC CTC TAC TTT GTC TTA GCT GTT AAA CTG TTT TTA GTA TTT TTG TTA   105
Gly Leu Tyr Phe Val Leu Ala Val Lys Leu Phe Leu Val Phe Leu Leu
    -20             -15             -10

AAT ATT TGC AAA GGG ATC GTG                                       126
Asn Ile Cys Lys Gly Ile Val
 -5                  1
```

```
(2) INFORMATION FOR SEQ ID NO: 157:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 383 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: CDNA

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 246..347
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:   score 3.6
                               seq IKCSSWISSLASG/IP

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:
```

```
AGTATTGAGT TGGAAGTGCC CATTGGACAT CACGTGGAGA TGAAATAGGC AATTAAAATA    60
```

TTCAGATCTT GGGTTCAGGA GCGAGACCCA TGTCTGAAAT ATAAACTTGC TCACTGTCAG   120

CCTGTGATGG TCTTTGTGAG ACATAGAATG AATATTAATA AAGAGGTGTA AGGACTGATC   180

CTGGGATCAT CCACAGTAAG GCTGGGGGAA GAGGAGACCT GGCAAAGGAA TCAAAGACAT   240

GATCC ATG AGG AAG AAG CGA GTR GAA GAA CTA ATA GTG TTT CCA GGA GAA   290
      Met Arg Lys Lys Arg Val Glu Glu Leu Ile Val Phe Pro Gly Glu
          -30   -25   -20

GTA ACT TCT TTC TCC TCC ATC AAG TGC TCC TCT TGG ATT TCT TCC CTG   338
Val Thr Ser Phe Ser Ser Ile Lys Cys Ser Ser Trp Ile Ser Ser Leu
        -15   -10   -5

GCT TCT GGA ATA CCA CAC TCT CTT GGA TTC TCC CTT CCC CCA GGG   383
Ala Ser Gly Ile Pro His Ser Leu Gly Phe Ser Leu Pro Pro Gly
        1   5   10

(2) INFORMATION FOR SEQ ID NO: 158:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 427 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 257..340
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.6
                                    seq ACLFSXFLAVSRH/PN

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AAGAACCCTT TTTATAGATA GGTCTTGTCT GGATTTGTGC ACGTGGATTT ATAATGAGAG   60

ATTTTCTAGT TGTTTTTGGT TCTCCTCCTC CTCCTCCTCC TTTDHCCTCC TTCTVTTCCT   120

CCTTTTCTTC CTCCTTWTCT TCTAAAACCT CTAATCTCTT ATTCCCTCTA ATGTCTGACC   180

AAAGTACTGC TGTCTGAGAC ATTGGAGGCA TACTGTGCTC CTCTTCTTCC CTCCCTGTGG   240

AGAAGCCTTA AGTTAT ATG CCT TCA TCC AGT CTT GCA GAG TTG TGT CTA ATG   292
              Met Pro Ser Ser Ser Leu Ala Glu Leu Cys Leu Met
                  -25   -20

CAG CAA GAT GCC TGC CTG TTT TCT KTG TTC CTA GCW GTC TCC AGG CAT   340
Gln Gln Asp Ala Cys Leu Phe Ser Xaa Phe Leu Ala Val Ser Arg His
    -15   -10   -5

```
CCA AAC TAT NVK TGT TCC ATC AGT ACT AAG GGT GAG GTG AGA GAG AAA    388
Pro Asn Tyr Xaa Cys Ser Ile Ser Thr Lys Gly Glu Val Arg Glu Lys
 1               5                  10                  15

CTA GTT CCT TGG ATA ACA CAC CAA ATG GCC AGA ATG TTG              427
Leu Val Pro Trp Ile Thr His Gln Met Ala Arg Met Leu
            20                  25
```

(2) INFORMATION FOR SEQ ID NO: 159:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 158 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 21..140
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                        seq LQMRMQLPCLVLG/EE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```
AATTTTCAGT AGGAAACATT ATG GAT CTG TGG AGC TGC TTA TTT CCA GTG ATG    53
                      Met Asp Leu Trp Ser Cys Leu Phe Pro Val Met
                      -40                 -35                 -30

CTG ATG GAG CCA TCC AAA GGG CTG GAA GAT TCA GAG TGG AAA ATG GCT    101
Leu Met Glu Pro Ser Lys Gly Leu Glu Asp Ser Glu Trp Lys Met Ala
            -25                 -20                 -15

CTT CAG ATG AGA ATG CAA CTG CCC TGC CTG GTA CTT GGC GAA GAA CAG    149
Leu Gln Met Arg Met Gln Leu Pro Cys Leu Val Leu Gly Glu Glu Gln
        -10                 -5                   1

ACG CTT GGG                                                        158
Thr Leu Gly
 5
```

(2) INFORMATION FOR SEQ ID NO: 160:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 319 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

```
    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 209..289
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 3.6
                          seq AVPLPTTSTLTSA/ST

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:


AAGTTCTGTG GGCTCTATTC GGCCATATTA ATAAAGAGAA AGGGAAGGCT GACHGTCCTT     60

CGCCTCCGCC CCCACATACA CACCCCTTCT TCCCACTCCG CTCTCACGAC TAAGCTCTCA    120

CGATTAAGGC ACGCCTGCCT CGATTGTCCA GCCTCTGCCA GAAGAAAGCT TAGCAGCCAG    180

CGCCTCAGTA GAGACCTAAG GGCGCTGA ATG AGT GGG AAA GGG AAA TGC CGA       232
                                  Met Ser Gly Lys Gly Lys Cys Arg
                                      -25                 -20

CCA ATT GCG CTG CGG CGG GCT GTG CCA TTA CCT ACA ACA AGC ACA TTA      280
Pro Ile Ala Leu Arg Arg Ala Val Pro Leu Pro Thr Thr Ser Thr Leu
        -15             -10             -5

ACA TCA GCT TCC ACA GGT TTC CTT TGG ATC CTA AAA GAA                  319
Thr Ser Ala Ser Thr Gly Phe Leu Trp Ile Leu Lys Glu
    1           5               10



(2) INFORMATION FOR SEQ ID NO: 161:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 91 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 14..67
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 3.6
                             seq IQKSSGLFCPSQA/QS

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:


AGAAAATGGA AAA ATG ACC CCA AAG GCA ATT CAG AAA TCA TCA GGG CTC       49
            Met Thr Pro Lys Ala Ile Gln Lys Ser Ser Gly Leu
```

```
                          -15                    -10
TTC TGC CCA TCA CAG GCC CAG AGC GCA AGA CCC GCA GAA AAG                91
Phe Cys Pro Ser Gln Ala Gln Ser Ala Arg Pro Ala Glu Lys
    -5                    1                   5
```

(2) INFORMATION FOR SEQ ID NO: 162:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 364 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 56..271
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                            seq CTSLLQLYDASNS/EW

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```
AAACTCGCTG GGCTCCAAAA GAAACACTGG CTTCTCTCCT TCAGCTCCAG GCTAG ATG     58
                                                              Met

CCA GAC CAG TTT GAC CAG GCG GTT GTG CTG AAC CAG CTG CGG TAC TCA    106
Pro Asp Gln Phe Asp Gln Ala Val Val Leu Asn Gln Leu Arg Tyr Ser
    -70                 -65                 -60

GGG ATG CTG GAG ACT GTG AGA ATC CGC AAA GCT GGG TAT GCG GTC CGA    154
Gly Met Leu Glu Thr Val Arg Ile Arg Lys Ala Gly Tyr Ala Val Arg
-55                 -50                 -45                 -40

AGA CCC TTT CAG GAC TTT TAC AAA AGG TAT AAA GTG CTG ATG AGG AAT    202
Arg Pro Phe Gln Asp Phe Tyr Lys Arg Tyr Lys Val Leu Met Arg Asn
                -35                 -30                 -25

CTG GCT CTG CCT GAG GAC GTC CGA GGG AAG TGC ACG AGC CTG CTG CAG    250
Leu Ala Leu Pro Glu Asp Val Arg Gly Lys Cys Thr Ser Leu Leu Gln
            -20                 -15                 -10

CTC TAT GAT GCC TCC AAC AGC GAG TGG CAG CTG GGG AAG ACC AAG GTC    298
Leu Tyr Asp Ala Ser Asn Ser Glu Trp Gln Leu Gly Lys Thr Lys Val
        -5                  1                   5

TTT CTT CGA GAA TCC TTG GAA CAG AAA CTG GAG AAG CGG AGG GAA GAG    346
Phe Leu Arg Glu Ser Leu Glu Gln Lys Leu Glu Lys Arg Arg Glu Glu
10                  15                  20                  25

GAA GTG AGC CAC GCT GGG                                            364
Glu Val Ser His Ala Gly
```

30

(2) INFORMATION FOR SEQ ID NO: 163:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 185 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 129..173
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                      seq LVSFFLELNVLQQ/WP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:


```
AGTAGACCGC GCACTGGAAG GCGTGCGCGC AGGTGTGCGT GACCATGTGC TTGAAACGGC   60

AGTAGCGCAS RNGNAAGGAT CGCCATCACA CGGCGCACTG GTGCGGCTTC TCCCCCGAGT  120

GGACGAAC ATG TGC TTG GTG TCG TTT TTC CTT GAG CTG AAC GTC TTG CAA  170
         Met Cys Leu Val Ser Phe Phe Leu Glu Leu Asn Val Leu Gln
         -15               -10                 -5

CAG TGG CCG GCA GGG                                                185
Gln Trp Pro Ala Gly
    1
```


(2) INFORMATION FOR SEQ ID NO: 164:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 234 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 103..141
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6

seq MRSLACLTPCGHA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

ATACCTCTTC CAGTTGGGAA AAAATGGACT TAAAATGTCC CATGTCCAGG CTGACCTGGA   60

TGATGACAGT TGGTTGATGA GTTAATTTGA ACATGAGCAG AA ATG AGG TCA CTT   114
                                                     Met Arg Ser Leu
                                                               -10

GCC TGC CTG ACT CCA TGT GGC CAT GCT GGC TCC AGG TTG CAA AGT TCT   162
Ala Cys Leu Thr Pro Cys Gly His Ala Gly Ser Arg Leu Gln Ser Ser
         -5   1   5

TTG AGC AAG TAC CTT GTC TTG CCT AAT CTC GAA TGT CTG TTC TTT TTA   210
Leu Ser Lys Tyr Leu Val Leu Pro Asn Leu Glu Cys Leu Phe Phe Leu
      10   15   20

TTT CTT ATC TCA AAT AGG CGC TGG   234
Phe Leu Ile Ser Asn Arg Arg Trp
   25   30

(2) INFORMATION FOR SEQ ID NO: 165:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 315 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 70..108
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                                seq MHLLSNWANPASS/RR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

AAGTGGCCAT GGCGGATACA GCGACTACAG CATCGGCGGC GGCGGCTAGT GCCGCTAGCG   60

CCTCGAGCG ATG CAC CTC CTT TCC AAC TGG GCA AAC CCC GCT TCC AGC AGA   111
        Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
             -10   -5   1

CGT CCT TCT ATG GCC GCT TCA GGC ACT TCT TGG ATA TCA TCG ACC CTC   159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
      5   10   15

GCA CAC TCT TTG TCA CTG AGA GAC GTC TCA GAG AGG CTG TGC AGC TGC   207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys

```
                    20                      25                      30
TGG AGG ACT ATA AGC ATG GGA CCC TGC GCC CGG GGG TCA CCA ATG AAC        255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
    35                      40                      45

AGC TCT GGA GTG CAC AGA AAA TCA AGC AGG CTA TTC TAC ATC CGG ACA        303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
50                      55                      60                      65

CCA ATG AGA AGA                                                         315
Pro Met Arg Arg
```

(2) INFORMATION FOR SEQ ID NO: 166:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 415 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 62..133
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                                 seq FAMLHSVWRLIPA/FR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```
AAAGGAGCCA ACYKCACAGT ACATTTCTCT TTGTCATGAA TTGCATACTT TGTTCCAAGT         60

C ATG TGG TCT GGA AAG TGG GCG TTG GTC TCA CCA TTT GCT ATG CTA CAC        109
  Met Trp Ser Gly Lys Trp Ala Leu Val Ser Pro Phe Ala Met Leu His
      -20                     -15                     -10

TCA GTG TGG AGA CTC ATT CCT GCC TTT CGT GGT TAC GCC CAA CAA GAC        157
Ser Val Trp Arg Leu Ile Pro Ala Phe Arg Gly Tyr Ala Gln Gln Asp
        -5                      1                       5

GCT CAG GAA TTT CTT TGT GAA CTT TTA GAT AAA ATA CAA CGT GAA TTA        205
Ala Gln Glu Phe Leu Cys Glu Leu Leu Asp Lys Ile Gln Arg Glu Leu
    10                      15                      20

GAG ACA ACT GGT ACC AGT TTA CCA GCT CTT ATC CCC ACT TCT CAA AGG        253
Glu Thr Thr Gly Thr Ser Leu Pro Ala Leu Ile Pro Thr Ser Gln Arg
25                      30                      35                      40

AAA CTC ATC AAA CAA GTT CTG AAT GTT GTA AAT AAC ATT TTT CAT GGA        301
Lys Leu Ile Lys Gln Val Leu Asn Val Val Asn Asn Ile Phe His Gly
            45                      50                      55
```

```
CAA CTT CTT AGT CAG GTT ACA TGT CTT GCA TGT GAC AAC AAA TCA AAT    349
Gln Leu Leu Ser Gln Val Thr Cys Leu Ala Cys Asp Asn Lys Ser Asn
            60                  65                  70

ACC ATA GAA CCT TTC TGG GAC TTG TCA TTG GAG TYT CCA GAA AGG TAT    397
Thr Ile Glu Pro Phe Trp Asp Leu Ser Leu Glu Xaa Pro Glu Arg Tyr
            75                  80                  85

CAA TGC AGT NGA AAA GGG                                             415
Gln Cys Ser Xaa Lys Gly
        90
```

(2) INFORMATION FOR SEQ ID NO: 167:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 130..189
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                            seq KFCLICLLTFIFH/HC

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
AAGACGCGCC GGTTTCTGCG ACGCAGTTAG CGCAGTCTGC TTTGGTGAAT ACACGATTTG    60

GTGCAGCCGG GGTTTGGTAC CGAGCGGAGA GGAGATGCAC ACGGCACTCG AGTGTGAGGA   120

AAAATAGAA ATG AAG GTA CAT ATG CAC ACA AAA TTT TGC CTC ATT TGT TTG   171
           Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu
           -20                 -15                 -10

CTG ACA TTT ATT TTT CAT CAT TGC AAC CAT TGC CAT GAA GAA CAT GAC    219
Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp
 -5                   1                   5                   10

CAT GGC CCT GAA GCG CTT CAC AGA CAG CAA GGG                        252
His Gly Pro Glu Ala Leu His Arg Gln Gln Gly
            15                  20
```

(2) INFORMATION FOR SEQ ID NO: 168:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 436 base pairs
        (B) TYPE: NUCLEIC ACID

```
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 290..361
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 3.5
                                    seq ALSLFYTADTSHG/SE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:
```

```
ATATTTCTTG TCAACAGTAT TGAAATGTAA TATGTATGTG TTCATGTATG AGMAATTTTT    60

ACTCCACACA GGTGTTTCAG TAGAGTGGGG CAGGAAAAGA GATCTCTTCG ATTTCTTTCA   120

GGCCTGAGGC TTTTGTGAAA TGCGTCASCC CCTGTGACAG TAGGTTTTGA TGCTAGTGAT   180

CTTCAGATCT TTCTCTCTGG AAATGTGCAG AGAGTGTCAG TTTCCCAAGT TCTGAGGTAA   240

CTCTCAGCCC AGATGTGAAA TGGGAGCCTA CCAGCTGGTA TAGAAGGGA ATG GGT AGG   298
                                                       Met Gly Arg

AGG CAC TGG GTG CTG ACT CAT TCA GCA CTG TCC CTT TTC TAT ACT GCT   346
Arg His Trp Val Leu Thr His Ser Ala Leu Ser Leu Phe Tyr Thr Ala
   -20               -15               -10

GAT ACA TCC CAT GGT TCT GAG AAG CCT TAT CTC AGT CTA TTT GGA AGA   394
Asp Thr Ser His Gly Ser Glu Lys Pro Tyr Leu Ser Leu Phe Gly Arg
 -5                 1               5                 10

GAG GGA GGW AGA GAA GGR AGT AAC CCA AAG TAC TAC TCA TTT           436
Glu Gly Gly Arg Glu Gly Ser Asn Pro Lys Tyr Tyr Ser Phe
             15                 20                 25
```

```
(2) INFORMATION FOR SEQ ID NO: 169:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 343 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 104..336
```

        .(C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 1..233
                                id H07998
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 110..336
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 1..227
                                id W37530
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 110..336
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 1..227
                                id R79812
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 110..336
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 1..227
                                id N24900
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 110..336
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 1..227
                                id R34849
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 65..112
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 12.5
                                seq FVVLLALVAGVLG/NE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ATGTCGCCCG TGTCCCGCCG GCCCGTTCCG TGTCGCCCCG CAGTGYTGCG GCCGCCGCKK   60

CACC ATG GCT GTG TTT GTC GTG CTC CTG GCG TTG GTG GCG GGT GTT TTG   109
     Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu
      -15   -10   -5

GGG AAC GAG TTT AGT ATA TTA AAA TCA CCA GGG TCT GTT GTT TTC CGA   157
Gly Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg
     1   5   10   15

```
AAT GGA AAT TGG CCT ATA CCA GGA GAG CGG ATC CCA GAC GTG GCT GCA    205
Asn Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala
            20                  25                  30

TTG TCC ATG GGC TTC TCT GTG AAA GAA GAC CTT TCT TGG CCA GGA CTC    253
Leu Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu
            35                  40                  45

GCA GTG GGT AAC CTG TTT CAT CGT CCT CGG GCT AGC GTC ATG GTG ATG    301
Ala Val Gly Asn Leu Phe His Arg Pro Arg Ala Ser Val Met Val Met
            50                  55                  60

GTG AAG GGA GTT AAC AAC TMC CCT CTA CCC CCA NGN TGG NGG            343
Val Lys Gly Val Asn Asn Xaa Pro Leu Pro Pro Xaa Trp Xaa
    65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO: 170:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 234 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 111..209
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 90
                                region 1..99
                                id N50844
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 186..232
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 93
                                region 75..121
                                id N50844
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 111..209
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 90
                                region 1..99
                                id N29905
                                est

    (ix) FEATURE:

```
            (A) NAME/KEY: other
            (B) LOCATION: 186..232
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 93
                                    region 75..121
                                    id N29905
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 186..232
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 93
                                    region 75..121
                                    id N62597
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 186..232
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 93
                                    region 76..122
                                    id R80247
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 186..232
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 93
                                    region 76..122
                                    id H03409
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 40..87
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 10.1
                                    seq LLLQLAVLGAALA/AA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:


AAGAGGTGCG GGATTGGGCG GGCTGCCACG GCATGGAGA ATG GCT CCG CTT CTG        54
                                          Met Ala Pro Leu Leu
                                                          -15

TTG CAG CTG GCG GTG CTC GGC GCG GCG CTG GCG GCC GCA GCC CTC GTA       102
Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala Ala Ala Ala Leu Val
    -10              -5                   1               5

CTG ATT TCC ATC GTT GCA TTT ACA ACT GCT ACA AAA ATG CCA GCA CTC      150
Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr Lys Met Pro Ala Leu
                10               15                   20

CAT CGA CAT GAA GAA CAG AAA TTC TTC TTA AAT GCC AAA GGC CAG AAA      198
His Arg His Glu Glu Gln Lys Phe Phe Leu Asn Ala Lys Gly Gln Lys
                25               30                   35
```

GAA ACT TTA CCC AGC ATA TGG GAC TCA CCT ACC AGG   234
Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr Arg
        40   45

(2) INFORMATION FOR SEQ ID NO: 171:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 386 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 52..228
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 94
                                        region 1..177
                                        id AA074050
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 266..387
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 99
                                        region 218..339
                                        id AA074050
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 135..284
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 9.8
                                        seq LLRLLQLVSTCVA/FS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

AGCGGCCGCA GCCAGCCAGG CCGCGCMMGG GACGACTGCA GAGCGCGGTG CTCTTACAGC   60

CTGTTCCAAG TGTGGCTTAA TCCGTCTCCA CCACCAGATC TTTCTCCGTG GATTCCTCTG   120

CTAAGACCGC TGCC ATG CCA GTG ACG GTA ACC CGC ACC ACC ATC ACA ACC   170
                Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr
                -50   -45   -40

ACC ACG ACG TCA TCT TCG GGC CTG GGG TCC CCC ATG ATC GTG GGG TCC   218
Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser
            -35   -30   -25

CCT CGG GCC CTG ACA CAG CCC CTG GGT CTC CTT CGC CTG CTG CAG CTG   266

Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu
    -20   -15   -10

GTG TCT ACC TGC GTG GCC TTC TCG CTG GTG GCT AGC GTG GGC GCC TGG   314
Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
    -5   1   5   10

ACG GGG TCC ATG GGC AAC TGG TCC ATG TTC ACC TGG TGC TTC TGC TTC   362
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe
                15   20   25

TCN GTG ACC CTG ATC ATC CTC ATC   386
Ser Val Thr Leu Ile Ile Leu Ile
        30

(2) INFORMATION FOR SEQ ID NO: 172:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 326 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 147..290
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                   region 57..200
                                   id W40499
                                   est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 90..151
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                   region 1..62
                                   id W40499
                                   est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 100..319
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                   region 46..265
                                   id R88049
                                   est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 100..319

```
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 56..275
                                id T08712
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 100..319
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 32..251
                                id H38484
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 147..319
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 65..237
                                id T65344
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 102..151
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 21..70
                                id T65344
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 111..164
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 9.2
                                seq VFLCSLLAPMVLA/SA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:


AGACTCTTGG GGACTGGGCT GAGGACGGGG TGGTACTGCT CCTGGCAGGG CCAGAGGTGG    60


ATGGGGCTTG AAAAGGGGGT TCAAGGCAGC AGMTCTATGG TTCAGACGCC ATG GAG       116
                                                         Met Glu


TTG GTG CTG GTC TTC CTC TGC AGC CTG CTG GCC CCC ATG GTC CTG GCC     164
Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val Leu Ala
    -15                 -10                 -5


AGT GCA GCT GAA AAG GAG AAG GAA ATG GAC CCT TTT CAT TAT GAT TAC     212
Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr Asp Tyr
  1               5                10                  15


CAG ACC CTG AGG ATT GGG GGA CTG GTG TTC GCT GTG GTC CTC TTC TCG     260
Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu Phe Ser
              20                25                  30


GTT GGG ATC CTC CTT ATC CTA AGT CGC AGG TGC AAG TGC AGT TTC AAT     308
```

Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser Phe Asn
      35   40   45

CAG AAG CCC CGC AAC AGA   326
Gln Lys Pro Arg Asn Arg
    50

(2) INFORMATION FOR SEQ ID NO: 173:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 376 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 74..344
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                               region 73..343
                               id H95186
                               est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 25..86
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 93
                               region 25..86
                               id H95186
                               est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 138..377
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                               region 1..240
                               id N40665
                               est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 203..308
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                               region 230..335
                               id W25197
                               est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide

            (B) LOCATION: 167..304
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.9
                                    seq LLGLLSAEQLAEA/SV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

AACGGGCGTC GGGAAGACGC TGCTGGTGAA ACGGCTGCAG GAGGTGAGCT CCCGGGATGG   60

GAAAGGCGAC CTGGGGGAGC CGCCCCCGAC ACGGCCCACG GTGGGCACCA ATCTTACTGA   120

CATCGTGGCA CAGAGAAAGA TCACCATCCG GGAGCTTGGG GGGTGC ATG GGC CCC   175
                                                     Met Gly Pro
                                                     -45

ATC TGG TCC AGT TAC TAT GGA AAC TGC CGT TCT CTC CTG TTT GTG ATG   223
Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val Met
            -40   -35   -30

GAC GCC TCT GAC CCC ACC CAG CTC TCT GCA TCC TGT GTG CAG CTC TTA   271
Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu Leu
            -25   -20   -15

GGT CTC CTT TCT GCA GAA CAA CTT GCA GAA GCA TCG GTG CTG ATA CTC   319
Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile Leu
            -10   -5   1   5

TTC AAT AAA ATC GAC CTA CCC TGT TAC ATG TCC ACG GAG GAG ATG AAG   367
Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met Lys
                 10   15   20

TCA TTA ATC   376
Ser Leu Ile

(2) INFORMATION FOR SEQ ID NO: 174:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 277 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 59..278
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 97
                                    region 28..247
                                    id R78970
                                    est

        (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 59..210
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                               region 29..180
                               id R64509
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 196..278
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                               region 167..249
                               id R64509
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 59..210
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                               region 44..195
                               id H85714
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 196..278
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                               region 182..264
                               id H85714
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 59..278
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                               region 36..255
                               id H52756
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 59..278
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                               region 5..224
                               id H49758
                               est

(ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 107..247
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7.9
                               seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:
```

```
ATCACGTGGC RGCCACCCAG GKAMGAAGAR NANVTCTTCC TGGGGTTVHT TCTCCGANRT    60

GACGTSYSGC CTTTGAGATC AACTCTCCTG TACCAGCGTA GGCCGC ATG AGT GGG      115
                                                    Met Ser Gly
                                                        -45

GGG CGG GCT CCC GCG GTC CTG CTC GGC GGA GTG GCC TCT CTG CTC CTG    163
Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser Leu Leu Leu
            -40              -35              -30

TCT TTT GTT TGG ATG CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG    211
Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu
            -25              -20              -15

TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC    259
Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr
            -10               -5                1

CAG CCC TCG CCG GCC TGG                                             277
Gln Pro Ser Pro Ala Trp
  5                  10
```


(2) INFORMATION FOR SEQ ID NO: 175:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 388 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 180..390
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                    region 134..344
                                    id H08480
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 115..185
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 100
                                    region 1..71
                                    id H08480
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 113..232

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
                        seq SLLLLFGGQFASS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:


```
AGCAGAGCTT CCGCTTCCGG CCCTTCAGGC TCTGTCTCTG TGGAGACTGG GCTTTGGGAG    60

GKAGAAAGAG GGACCTAGCG CGGGCCGCGC AGGCGCACGG TGGGCAGCTG CA ATG GCG   118
                                                          Met Ala
                                                          -40

CTG TCG TGT ACC CTT AAC AGG TAT CTG CTC CTC ATG GCG CAG GAG CAT    166
Leu Ser Cys Thr Leu Asn Arg Tyr Leu Leu Leu Met Ala Gln Glu His
        -35                 -30                 -25

CTG GAG TTC CGC CTG CCG GAA ATA RRG TCT TTG CTT TTG CTT TTT GGA    214
Leu Glu Phe Arg Leu Pro Glu Ile Xaa Ser Leu Leu Leu Leu Phe Gly
        -20                 -15                 -10

GGT CAG TTT GCC AGC AGT CAA GAA ACT TAT GGA AAG TCA CCA TTT TGG    262
Gly Gln Phe Ala Ser Ser Gln Glu Thr Tyr Gly Lys Ser Pro Phe Trp
        -5              1               5               10

ATT CTT AGC ATT CCC TCT GAA GAT ATT GCA AGA AAT TTG ATG AAA CGG    310
Ile Leu Ser Ile Pro Ser Glu Asp Ile Ala Arg Asn Leu Met Lys Arg
                15              20              25

ACA GTG TGT GCC AAG TCT ATA TTT GAA CTA TGG GGT CAT GGA CAA TCT    358
Thr Val Cys Ala Lys Ser Ile Phe Glu Leu Trp Gly His Gly Gln Ser
        30              35              40

CCT GAG GAG CTG TAC AGT TCT CTT AAA AAC                            388
Pro Glu Glu Leu Tyr Ser Ser Leu Lys Asn
        45              50
```


(2) INFORMATION FOR SEQ ID NO: 176:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 311 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 112..309
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 97
                                   region 69..266
                                   id AA149265
                                   est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 41..86
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                       region 1..46
                       id AA149265
                       est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 110..309
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                       region 53..252
                       id W39570
                       est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 56..86
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 96
                       region 2..32
                       id W39570
                       est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 110..309
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                       region 55..254
                       id N41332
                       est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 53..86
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                       region 1..34
                       id N41332
                       est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 39..197
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 7.1
                       seq IAVGLGVAALAFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```
AACTGCCGCG GCGCCTTGAG TCTCCGGGCC GCCTTGCC ATG GCT GCC CGT GGT GTC   56
                                          Met Ala Ala Arg Gly Val
                                                              -50

ATC GCT TCA GTT GGC GAG AGT TTG CGC TAC GCT GAG TAC TTG CAG CCC      104
```

```
Ile Ala Pro Val Gly Glu Ser Leu Arg Tyr Ala Glu Tyr Leu Gln Pro
    -45                 -40                 -35

TCG GCC AAA CGG CCA GAC GCC GAC GTC GAC CAG CAG AGA CTG GTA AGA    152
Ser Ala Lys Arg Pro Asp Ala Asp Val Asp Gln Gln Arg Leu Val Arg
    -30                 -25                 -20

AGT TTG ATA GCT GTA GGA CTG GGT GTT GCA GCT CTT GCA TTT GCA GGT    200
Ser Leu Ile Ala Val Gly Leu Gly Val Ala Ala Leu Ala Phe Ala Gly
-15                 -10                 -5                      1

CGC TAC GCA TTT CGG ATC TGG AAA CCT CTA GAA CAA GTT ATC ACA GAA    248
Arg Tyr Ala Phe Arg Ile Trp Lys Pro Leu Glu Gln Val Ile Thr Glu
            5                 10                 15

ACT GCA AAG AAG ATT TCA ACT CCT AGC TTT TCA TCC TAC TAT AAA GGA    296
Thr Ala Lys Lys Ile Ser Thr Pro Ser Phe Ser Ser Tyr Tyr Lys Gly
        20                 25                 30

GGA TTT GAA CGG AGG                                               311
Gly Phe Glu Arg Arg
    35
```


(2) INFORMATION FOR SEQ ID NO: 177:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 384 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 43..87
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                                region 8..52
                                id W32101
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 89..129
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                                region 53..93
                                id W32101
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 292..375
        (C) IDENTIFICATION METHOD: Von Heijne matrix

        (D) OTHER INFORMATION: score 6.6
                                seq VLGXLFLGGLCRG/WD

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

AAGAGCCGCG TTYAGTCTAT CGCTGCGGTT GCGAGCGCTG TAGGGAGCCT GTGCTGTGCC   60

GCGCAGTTAG GCAGCAGCAG CCGCGGAGCA GTAGCCGCCG TGGGAGGGAG CCATGAAGCA   120

TTACGAGGTA AGAAGCGAGA AACAGGGGCC GTGTGGCCAC TGCTGACCCA TTCTTTTTCC   180

TTCTTTGCGG GACCACGGGA CCCCACTTTC TGGTCCTGTG CCCCGAAGGA AGAKCCAGAC   240

GGCGCAGGCG CAGTGGGCAA GCGTTGCGCC CCGGGCCACT CGTAAATTCC A ATG CGC   297
                                                          Met Arg

ATG TGC GCA GGA AGT ATT TAT AAA TCT GCA ACC CAG GCT GTT TTG GGG   345
Met Cys Ala Gly Ser Ile Tyr Lys Ser Ala Thr Gln Ala Val Leu Gly
    -25   -20   -15

GWA CTT TTT CTT GGG GGT CTC TGC AGG GGC TGG GAC GCT   384
Xaa Leu Phe Leu Gly Gly Leu Cys Arg Gly Trp Asp Ala
-10   -5   1

(2) INFORMATION FOR SEQ ID NO: 178:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 425 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 73..317
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                region 1..245
                                id HUM506F10B
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 314..376
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                                region 243..305
                                id HUM506F10B
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other

```
        (B) LOCATION: 63..193
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                                region 1..131
                                id AA056148
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 314..401
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                                region 254..341
                                id AA056148
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 277..317
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                region 216..256
                                id AA056148
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 397..426
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 338..367
                                id AA056148
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 88..189
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                                region 1..102
                                id HSC1FF051
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 314..401
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 230..317
                                id HSC1FF051
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 187..271
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                                region 101..185
                                id HSC1FF051
                                est
```

```
(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 269..317
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 93
                              region 184..232
                              id HSC1FF051
                              est


(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 397..426
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 96
                              region 314..343
                              id HSC1FF051
                              est


(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 87..200
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 92
                              region 1..114
                              id HSC16E081
                              est


(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 314..401
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 96
                              region 231..318
                              id HSC16E081
                              est


(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 199..275
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 94
                              region 114..190
                              id HSC16E081
                              est


(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 269..317
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 91
                              region 185..233
                              id HSC16E081
                              est


(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 397..426
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 96
                              region 315..344
                              id HSC16E081
```

```
                                    est

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 85..186
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 99
                                 region 24..125
                                 id AA157365
                                 est

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 183..263
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 90
                                 region 123..203
                                 id AA157365
                                 est

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 337..401
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 95
                                 region 278..342
                                 id AA157365
                                 est

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 273..326
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 90
                                 region 213..266
                                 id AA157365
                                 est

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 186..419
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 6.3
                                 seq TLIMLLSWQLSVS/SV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:


AATGCGCGCT CGCGNTCCCG CCCTCTAGCT GCGCTCGGCT GAGTCAGTCA GTCTGTCGGA   60

GTCTGTCCTC GGAGCAGGCG GAGTAAAGGG ACTTGAGCGA GCCAGTTGCC GGATTATTCT  120

ATTTCCCCTC CCTCTCTCCC GCCCCGTATC TCTTTTCACC CTTCTCCCAC CCTCGCTCGC  180

GTASC ATG GCG GAG CGT CGG CGG CCA CTC AGT CCC ATT CCA TCT NNT CGT  230
      Met Ala Glu Arg Arg Arg Pro Leu Ser Pro Ile Pro Ser Xaa Arg
                -75                 -70                 -65

CGT CCT TCG GAG CCG AGC CGT CCG CGC CCG GCG GCG GCG GGA SCC AGG    273
Arg Pro Ser Glu Pro Ser Arg Pro Arg Pro Ala Ala Ala Gly Xaa Arg
          -60                 -55                 -50
```

```
AGC CTG CCC CGC CCT GGG GAC GAA GAG CTG CAG CTC CCC TGT GCG GTG      326
Ser Leu Pro Arg Pro Gly Asp Glu Glu Leu Gln Leu Pro Cys Ala Val
        -45             -40             -35
```

```
CAC GAT CTG ATT TTC TGG AGA GAT GTG AAG AAG ACT GGG TTT GTC TTT      374
His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly Phe Val Phe
    -30             -25             -20
```

```
GGC ACC ACG CTG ATC ATG CTG CTT TCC TGG CAG CTT TCA GTG TCA TCA      422
Gly Thr Thr Leu Ile Met Leu Leu Ser Trp Gln Leu Ser Val Ser Ser
-15             -10             -5              1
```

```
GTG                                                                  425
Val
```

(2) INFORMATION FOR SEQ ID NO: 179:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 403 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 105..351
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                         region 49..295
                         id R47336
                         est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 58..107
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                         region 1..50
                         id R47336
                         est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 352..381
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                         region 295..324
                         id R47336
                         est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide

        (B) LOCATION: 5..331
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6
                             seq LQLLLGMTASAVA/AL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

AAAG ATG GCG GCT CCC GTC CTG CTA AGA GTG TCG GTG CCG CGG TGG GAG   49
     Met Ala Ala Pro Val Leu Leu Arg Val Ser Val Pro Arg Trp Glu
                 -105   -100   -95

CGG GTG GCC CGG TAT GCA GTG TGC GCT GCC GGA ATC CTG CTC TCC ATC   97
Arg Val Ala Arg Tyr Ala Val Cys Ala Ala Gly Ile Leu Leu Ser Ile
             -90   -85   -80

TAC GCC TAC CAC GTG GAG CGG GAG AAG GAG CGG GAC CCC GAG CAC CGG   145
Tyr Ala Tyr His Val Glu Arg Glu Lys Glu Arg Asp Pro Glu His Arg
             -75   -70   -65

GCC CTC TGC GAC CTG GGG CCC TGG GTG AAG TGC TCC GCC GCC CTT GCC   193
Ala Leu Cys Asp Leu Gly Pro Trp Val Lys Cys Ser Ala Ala Leu Ala
             -60   -55   -50

TCC AGA TGG GGT CGA GGA TTT GGT CTT TTG GGT TCC ATT TTT GGA AAG   241
Ser Arg Trp Gly Arg Gly Phe Gly Leu Leu Gly Ser Ile Phe Gly Lys
     -45   -40   -35

GAT GGT GTA TTA AAC CAG CCA AAC AGT GTC TTT GGA CTT ATA TTT TAT   289
Asp Gly Val Leu Asn Gln Pro Asn Ser Val Phe Gly Leu Ile Phe Tyr
-30   -25   -20   -15

ATA CTA CAG TTA TTA CTT GGC ATG ACA GCA AGC GCT GTG GCG GCT TTG   337
Ile Leu Gln Leu Leu Leu Gly Met Thr Ala Ser Ala Val Ala Ala Leu
             -10   -5   1

ATC CTC ATG ACG TCC TCC ATC ATG TCG GTC GTG GGG TCC TGT ACC TGG   385
Ile Leu Met Thr Ser Ser Ile Met Ser Val Val Gly Ser Cys Thr Trp
         5   10   15

CCT ACA TTC TGT ACT ACG   403
Pro Thr Phe Cys Thr Thr
     20

(2) INFORMATION FOR SEQ ID NO: 180:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 367 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 112..260
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 92
                                region 121..269
                                id W31320
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 47..118
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 57..128
                                id W31320
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 273..333
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 282..342
                                id W31320
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 107..260
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 2..155
                                id T27259
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 273..369
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 168..264
                                id T27259
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 145..260
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 90
                                region 108..223
                                id AA157646
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 59..118
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 90
                                region 25..84
                                id AA157646
                                est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 273..307
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 94
                            region 245..279
                            id SSC8A04
                            est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 50..151
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 5.9
                            seq LGAAALALLLANT/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:
```

```
AATATACTTC TTTGTCAAGA GAAGCAGAGG TGTGGACGCT GTGTATGAA ATG TCT TTC     58
                                                          Met Ser Phe

CTC CAG GAC CCA AGT TTC TTC ACC ATG GGG ATG TGG TCC ATT GGT GCA     106
Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser Ile Gly Ala
    -30             -25             -20

GGA GCC CTG GGG GCT GCT GCC TTG GCA TTG CTG CTT GCC AAC ACA GAC     154
Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala Asn Thr Asp
-15             -10             -5               1

GTG TTT CTG TCC AAG CCC CWK AAA GCG GCC CTG GAG TAC CTG GAG GAT     202
Val Phe Leu Ser Lys Pro Xaa Lys Ala Ala Leu Glu Tyr Leu Glu Asp
            5               10              15

ATA GAC CTG AAA ACA CTG GAG AAG GAA CCA AGG ACT TTC AAA GCA AAG     250
Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys
            20              25              30

GAG CTA TGG GAA AAA AAT GGA GCT GTG ATT ATG GCC GTG CGG AGG CCA     298
Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val Arg Arg Pro
    35              40              45

GGC TGT TTC CTC TGT CGA GAG GAA GCT GCG GAT CTG TCC TCC CTG AAA     346
Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys
50              55              60              65

AGC ATG TTG GAC CAG CTG GGC                                          367
Ser Met Leu Asp Gln Leu Gly
                70
```

```
(2) INFORMATION FOR SEQ ID NO: 181:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 257 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR
```

```
(ii)  MOLECULE TYPE: CDNA

(vi)  ORIGINAL SOURCE:
      (A)  ORGANISM: Homo Sapiens
      (F)  TISSUE TYPE: Brain

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 138..257
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 98
                               region 83..202
                               id W31692
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 55..131
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 100
                               region 1..77
                               id W31692
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 136..257
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 98
                               region 78..199
                               id H50194
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 57..131
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 100
                               region 1..75
                               id H50194
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 57..257
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 97
                               region 1..201
                               id H46855
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 138..257
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 98
                               region 81..200
                               id H49687
                               est

(ix)  FEATURE:
```

          . (A) NAME/KEY: other
            (B) LOCATION: 57..132
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 100
                                    region 1..76
                                    id H49687
                                    est

     (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 138..257
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                    region 80..199
                                    id T54405
                                    est

     (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 58..124
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 100
                                    region 2..68
                                    id T54405
                                    est

     (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 90..200
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.9
                                    seq MLIMLGIFFNVHS/AV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATCTCTGCCC CCCTGCGAGG GCATCCTGGG CTTTCTCCCA CCGCTTTCCG AGCCCGCTTG   60

CACCTCGGCG ATCCCCGACT CCCTTCTTT ATG GCG TCG CTC CTG TGC TGT GGG   113
                                Met Ala Ser Leu Leu Cys Cys Gly
                                         -35   -30

CCG AAG CTG GCC GCC TGC GGC ATC GTC CTC AGC GCC TGG GGA GTG ATC   161
Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
              -25   -20   -15

ATG TTG ATA ATG CTC GGA ATA TTT TTC AAT GTC CAT TCC GCT GTG TTG   209
Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
              -10   -5   1

ATT GAG GAC GTT CCC TTC ACG GAG AAA GAT TTT GAG AAC GGC CCC CGG   257
Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Arg
  5   10   15

(2) INFORMATION FOR SEQ ID NO: 182:

     (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 400 base pairs
            (B) TYPE: NUCLEIC ACID

```
      (C) STRANDEDNESS: DOUBLE
      (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: CDNA

   (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Brain

   (ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 365..401
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 100
                              region 1..37
                              id R50224
                              est

   (ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 305..364
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 4.9
                              seq XSLFLHAVSSSFT/QL

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:
```

```
ATGACCACGG GTTTAACCTT CTTATCCCAG AGACACCCAA TTCTAGAGCT TTATGGAGCC     60

GTACTTCCCC CTGAATCCTA GCTCTAGGAC ATAGATCATG ACTCTCAGCC CTTTTACCCA    120

GGATGGAGCT GGGGCCTGTA TAGCCATATT ATTGTTCTAA GTAAGTTCTA GCCCCACCCT    180

CCCGCCTTCT TGAGTGATAC CTATTACGGA TGAGTTCTGG AAAAGACCCA GCTATGATTC    240

ATAAAAACAC TTCTGGATGA ATCAAGAACC ATTTCTTGTT TKTCCTAGAT AATTCTCTAA    300

AAAT ATG ATT CTT CCA TAT AGA ATG CKA AGC TTA TTT TTA CAT GCA GTT    349
     Met Ile Leu Pro Tyr Arg Met Xaa Ser Leu Phe Leu His Ala Val
     -20              -15                  -10

TCT AGC TCC TTC ACC CAG CTG AGG TCG TGC CAG GGA GAC AGA GTC TGG    397
Ser Ser Ser Phe Thr Gln Leu Arg Ser Cys Gln Gly Asp Arg Val Trp
 -5               1               5                   10

AGA                                                                 400
Arg
```

```
(2) INFORMATION FOR SEQ ID NO: 183:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 256 base pairs
      (B) TYPE: NUCLEIC ACID
      (C) STRANDEDNESS: DOUBLE
      (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: CDNA
```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 86..186
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 93
                            region 5..105
                            id AA096741
                            est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 23..211
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 4.8
                            seq LYTVRALAGRAWA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:


```
AGAAGTGCGT SYCGGCGGGA TC ATG GCG ACT TTG GTC GAA CTG CCG GAC TCG    52
                          Met Ala Thr Leu Val Glu Leu Pro Asp Ser
                          -60                     -55

GTC CTG CTC GAG ATC TTC TCT TAC CTC CCG GTA CGG GAC CGG ATC CGC    100
Val Leu Leu Glu Ile Phe Ser Tyr Leu Pro Val Arg Asp Arg Ile Arg
        -50                 -45                 -40

ATC TCC AGG GTC TGT CAC CGC TGG AAG AGG CTG GTG GAC GAC CGG TGG    148
Ile Ser Arg Val Cys His Arg Trp Lys Arg Leu Val Asp Asp Arg Trp
        -35                 -30                 -25

CTG TGG CGA CAT GTC GAC CTG ACG CTC TAC ACG GTA CGC GCA CTG GCC    196
Leu Trp Arg His Val Asp Leu Thr Leu Tyr Thr Val Arg Ala Leu Ala
        -20                 -15                 -10

GGG CGG GCC TGG GCC GCG GTC GCG GTG CCC GGA SCC CGA AGA CCA CCT    244
Gly Arg Ala Trp Ala Ala Val Ala Val Pro Gly Xaa Arg Arg Pro Pro
-5                  1                   5                   10

CTC CCA CCC TGG                                                    256
Leu Pro Pro Trp
        15
```


(2) INFORMATION FOR SEQ ID NO: 184:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 352 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

```
            (F) TISSUE TYPE: Brain

     (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 183..348
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 78..243
                                    id W52941
                                    est

     (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 286..348
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 96
                                    region 1..63
                                    id H55390
                                    est

     (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 77..199
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.7
                                    seq LFSCFCFLSHKFG/KK

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:
```

```
AAAAAATATC TCCCGGCGTG CGCTGCTTGT GTTATGTTCG GGTTTTAAGT CGTGTCAGCG      60

TTTACATTTT CTTAAT ATG AAA AAT GCC TGC ATT GTT CTG CCG CCA ACT CCC     112
              Met Lys Asn Ala Cys Ile Val Leu Pro Pro Thr Pro
              -40                -35                     -30

CCT CCC TCC CTG CAA CCC TCG GCC TCT CTG CTG GCG CCT AAT CGT TTT       160
Pro Pro Ser Leu Gln Pro Ser Ala Ser Leu Leu Ala Pro Asn Arg Phe
              -25                -20                     -15

TTA TTC TCT TGC TTC TGC TTT CTT AGT CAC AAG TTT GGG AAG AAA GTC       208
Leu Phe Ser Cys Phe Cys Phe Leu Ser His Lys Phe Gly Lys Lys Val
              -10                 -5                      1

ATC TAT TTC AAC TAC CTG AGT GAG CTC CAC GAA CAC CTT AAA TAC GAC       256
Ile Tyr Phe Asn Tyr Leu Ser Glu Leu His Glu His Leu Lys Tyr Asp
    5                   10                  15

CAG CTG GTC ATC CCT CCC GAA GTT TTG CGG TAC GAT GAG AAG CTC CAG       304
Gln Leu Val Ile Pro Pro Glu Val Leu Arg Tyr Asp Glu Lys Leu Gln
20                  25                  30                      35

AGC CTG CAC GAG GGC CGG ACG CCG MCT CCC ACC AAG ACA CCA CCA GGG       352
Ser Leu His Glu Gly Arg Thr Pro Xaa Pro Thr Lys Thr Pro Pro Gly
              40                  45                      50
```

```
(2) INFORMATION FOR SEQ ID NO: 185:

     (i) SEQUENCE CHARACTERISTICS:
```

```
          (A) LENGTH: 274 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 99..260
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 96
                                  region 126..287
                                  id T53519
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 40..108
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 91
                                  region 1..69
                                  id T53519
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 113..269
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 96
                                  region 131..287
                                  id W87344
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 147..269
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 96
                                  region 138..260
                                  id N56542
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 113..149
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 91
                                  region 105..141
                                  id N56542
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 75..105
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 96
```

region 1..31
id N56542
est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 113..218
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 96
                            region 117..222
                            id AA053475
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 218..269
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 94
                            region 223..274
                            id AA053475
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 113..269
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 95
                            region 90..246
                            id W05444
                            est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 110..193
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 4.6
                            seq PLQWSLLVAVVAG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:


```
ACTTCCGCCT GCGCCTGCGC AGCVCAGCTC CSHGAGCCCT GCCAACCATG GTGAACTTGG    60

GTCTGTCCCG GGTGGACGAC GCCGTGGCTG CCAAGCACCC GGCACCGGC ATG GCC TTT   118
                                                        Met Ala Phe

GGC TTG CAG ATG TTC ATT CAG AGG AAG TTT CCA TAC CCT TTG CAG TGG    166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp
-25                 -20             -15                 -10

AGC CTC CTA GTG GCC GTG GTT GCA GGC TCT GTG GTC AGC TAC GGG GTG    214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val
                 -5              1               5

ACG AGA GTR RAG TCG GAG AAA TGC AAC AAC CTC TGG CTC TTC CTG GAG    262
Thr Arg Val Xaa Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu
         10              15              20

ACC GGA CTT GGG                                                    274
Thr Gly Leu Gly
25
```

(2) INFORMATION FOR SEQ ID NO: 186:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 316 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 45..315
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                       region 1..271
                       id HSC1ZD051
                       est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 110..268
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.5
                       seq LLWTPLLSPGSLR/VI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

ATATGAGACT CTGGCCTCCC TGCAGATCTT CTAAGAACCA CACTAATGCA AGCGTGACAG   60

AGAAACCTCT TTCGAATGAC CTACTACAAC TCTGGCATTG GTTAGTTCC ATG TAT TGT   118
                                                    Met Tyr Cys

AAG ATT CTG GTG CTA ATG CTC CAT ACA GAA TTG ATC AGG ACT GAT TAC   166
Lys Ile Leu Val Leu Met Leu His Thr Glu Leu Ile Arg Thr Asp Tyr
-50   -45   -40   -35

TCT TCT GTG GAC CAA TTG CTA TTG AAC TAC CCA GCT GAA GAG GGT TTG   214
Ser Ser Val Asp Gln Leu Leu Leu Asn Tyr Pro Ala Glu Glu Gly Leu
          -30   -25   -20

GGG AGA GAA CGT TCA TTA TTA TGG ACT CCA CTT TTG TCS CCT GGT AGT   262
Gly Arg Glu Arg Ser Leu Leu Trp Thr Pro Leu Leu Ser Pro Gly Ser
        -15   -10   -5

TTA AGG GTG ATA CTA GAA TCC AGA GAA GTT CCT GTC TCC TTG TGG CCC   310
Leu Arg Val Ile Leu Glu Ser Arg Glu Val Pro Val Ser Leu Trp Pro
      1   5   10

CAA ACG   316
Gln Thr
15

(2) INFORMATION FOR SEQ ID NO: 187:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 423 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 50..246
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                            region 1..197
                            id AA043070
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 241..373
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                             region 191..323
                            id AA043070
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 371..408
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                             region 322..359
                            id AA043070
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 186..357
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                             region 29..200
                            id W81202
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 345..423
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                             region 189..267
                            id W81202
                            est

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 64..177
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 85..198
                             id W24858
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 178..227
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 198..247
                             id W24858
                             est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 166..243
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 4.5
                             seq ENSLIILLQGLQG/RV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```
AACTCTGCGC CCGGAGGACA GAGCGGCCCG GTCGCCGGCA TGGTTTCTCC GTCCTGCTGC   60

AGCCGGCGGG AGGCAGCCAG TCCAGGCGCC CGCTAGCTTC GGCGGCGACC CAGACGGGGA  120

AAGCGGAAGG AATGTCGCGT GCAAGCAGGC AGCTGGTGTG GAAGA ATG GCG GTG AGC  177
                                                   Met Ala Val Ser
                                                   -25

CAT TCA GTG AAG GAG CGG ACC ATC TCT GAG AAC AGC CTG ATC ATC CTA   225
His Ser Val Lys Glu Arg Thr Ile Ser Glu Asn Ser Leu Ile Ile Leu
    -20               -15               -10

CTG CAG GGC CTC CAG GGC CGG GTA ACC ACT GTG GAC CTG CGG GAT GAG   273
Leu Gln Gly Leu Gln Gly Arg Val Thr Thr Val Asp Leu Arg Asp Glu
    -5                1               5                   10

AGC GTG GCC CAC GGA CGC ATA GAC AAB GTC GAT GCT TTC ATG AAC ATC   321
Ser Val Ala His Gly Arg Ile Asp Xaa Val Asp Ala Phe Met Asn Ile
                15              20              25

CGC CTG GCC AAA GTC ACC TAC ACG GAC CGT TGG GGG CAT CAG GTC AAG   369
Arg Leu Ala Lys Val Thr Tyr Thr Asp Arg Trp Gly His Gln Val Lys
            30              35              40

CTG GAT GAC CTC TTT GTG ACA GGC CGC AAT GTC CGC TAC GTC CAC ATC   417
Leu Asp Asp Leu Phe Val Thr Gly Arg Asn Val Arg Tyr Val His Ile
            45              50              55

CCA GAT                                                            423
Pro Asp
    60
```

(2) INFORMATION FOR SEQ ID NO: 188:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 343 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 165..302
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 93
                                     region 33..170
                                     id T50032
                                     est

       (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 291..339
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 97
                                     region 160..208
                                     id T50032
                                     est

       (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 132..172
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 97
                                     region 1..41
                                     id T50032
                                     est

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 71..139
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 4.4
                                     seq QFILLGTTSVVTA/AL

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AAGGTGGAGA GTCGGGGGTC ACCAGGCCTA TCCTTGGCGC CACAGTCGGC CACCGGGGCT   60

CGCCGCCGTC ATG GAG AGC GGA GGG CGG CCC TCG CTG TGC CAG TTC ATC   109
            Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile
                  -20   -15

CTC CTG GGC ACC ACC TCT GTG GTC ACC GCC GCC CTG TAC TCC GTG TAC   157
Leu Leu Gly Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr
-10   -5   1   5

```
CGG CAG AAG GCC CGG GTC TCC CAA GAG CTC AAG GGA GCT AAA AAA GTT    205
Arg Gln Lys Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val
             10                  15                  20

CAT TTG GGT GAA GAT TTA AAG AGT ATT CTT TCA GAA GCT CCA GGA AAA    253
His Leu Gly Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys
         25                  30                  35

TGC GTG CCT TAT GCT GTT ATA GAA GGA GCT GTG CGG TCT GTT AAA GAA    301
Cys Val Pro Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu
     40                  45                  50

ACG CTT AAC AGC CAG TTT GTG GAA AAC TGC AAN GGG GTC CGG            343
Thr Leu Asn Ser Gln Phe Val Glu Asn Cys Xaa Gly Val Arg
55                  60                  65
```

(2) INFORMATION FOR SEQ ID NO: 189:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 481 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 133..355
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                 region 3..225
                                 id H10707
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 353..482
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                 region 224..353
                                 id H10707
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 154..354
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 93
                                 region 98..298
                                 id H30624
                                 est

    (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 368..403
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                               region 314..349
                               id H30624
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 200..354
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                               region 150..304
                               id HSC1VG011
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 111..198
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                               region 62..149
                               id HSC1VG011
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 49..85
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                               region 1..37
                               id HSC1VG011
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 202..344
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                               region 113..255
                               id R34406
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 111..198
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                               region 23..110
                               id R34406
                               est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 353..482
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                               region 115..244
                               id HSC23C111
                               est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 240..355
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 94
                            region 1..116
                            id HSC23C111
                            est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 56..472
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 4.3
                            seq GILVPHSLRQAQA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:


AAAAACTGCG GAGGGTGACA AGGAAGAAGG TGGCTCCAGA TCTGGAGGTG TGTCC ATG          58
                                                               Met


GCG GCG CTT GAC CTG CGA GCG GAS TGG ATT CGC TGG TCC TGC AGC TGC          106
Ala Ala Leu Asp Leu Arg Ala Xaa Trp Ile Arg Trp Ser Cys Ser Cys
        -135             -130             -125


TTG GGG GAM CTG GRA GGA GCT GGA GGG GAA ACG AAC GGT GTT GAA CGC          154
Leu Gly Xaa Leu Xaa Gly Ala Gly Gly Glu Thr Asn Gly Val Glu Arg
        -120             -115             -110


CCG GGT GGA GGA GGG CTG GCT CTC GCT CGC CAA GGC TCG CTA CGC GAT          202
Pro Gly Gly Gly Gly Leu Ala Leu Ala Arg Gln Gly Ser Leu Arg Asp
        -105             -100             -95


GGG CGC CAA GTC GGT AGG GCC CCT GCA GTA TGC TTC CCA CAT GGA GCC          250
Gly Arg Gln Val Gly Arg Ala Pro Ala Val Cys Phe Pro His Gly Ala
-90              -85              -80              -75


CCA GGT CTG CCT CCA CGC CAG CGA GDC YCA GGA GGG DST CCA GAA GTT          298
Pro Gly Leu Pro Pro Arg Gln Arg Xaa Xaa Gly Gly Xaa Pro Glu Val
        -70              -65              -60


CAA GGT GGT GAG AGC TGG TGT CCA CGC CCC AGA GGA GGT GGG GCC TCG          346
Gln Gly Gly Glu Ser Trp Cys Pro Arg Pro Arg Gly Gly Gly Ala Ser
        -55              -50              -45


CGA ACA GGT CTG CGG AGG CGC AAG GGC CCC ACT AAG ACC CCA GAA CCG          394
Arg Thr Gly Leu Arg Arg Arg Lys Gly Pro Thr Lys Thr Pro Glu Pro
        -40              -35              -30


GAG TCC TCT GAG GCC CCT CAG GAC CCC CTG AAC TGG TTT GGA ATC CTA          442
Glu Ser Ser Glu Ala Pro Gln Asp Pro Leu Asn Trp Phe Gly Ile Leu
    -25              -20              -15


GTT CCT CAC AGT CTA CGT CAG GCT CAA GCA AGC TTC CGG                      481
Val Pro His Ser Leu Arg Gln Ala Gln Ala Ser Phe Arg
-10              -5               1
```

(2) INFORMATION FOR SEQ ID NO: 190:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 302 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

     (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 176..275
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION: identity 100
                              region 2..101
                              id R68368
                              est

     (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 216..278
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 4.1
                              seq WWISLLPSLLSIC/KV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:


```
AAGCTTTCCC CGTGGTCTGA GTTTGTGGCT GCATTTTTAT CTCTGGTGGC TCTGCTACGG    60

CGGCGCAGAA ATGAGGCAGA AGCGGAAAGG AGATCTCAGC CCTGCTGAGC TGATGATGCT   120

GACTATAGGA GATGTTATTA AACAACTGAT TGAAGCCCAC GAGCAGGGGA AAGACATCGA   180

TCTAAATAAG GTGAAAACCA AGACAGCTGC CAAAT ATG GCC TTT CTG CCC AGC      233
                                     Met Ala Phe Leu Pro Ser
                                     -20

CCC GCC TGG TGG ATA TCA TTG CTG CCG TCC CTC CTC AGT ATC TGC AAG    281
Pro Ala Trp Trp Ile Ser Leu Leu Pro Ser Leu Leu Ser Ile Cys Lys
-15             -10             -5                          1

GTC TTG ATG CCC AAG TTA AAG                                         302
Val Leu Met Pro Lys Leu Lys
             5
```


(2) INFORMATION FOR SEQ ID NO: 191:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 414 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 40..271
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                            region 1..232
                            id R00384
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 294..328
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 94
                            region 257..291
                            id R00384
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 86..130
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 93
                            region 140..184
                            id MMTEST284
                            est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 34..180
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 3.8
                            seq PAFHLPLPGPTLA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AATTCCCCAG CAAGCTCAGC GTGTAMSTGC GCT ATG GAG CCG AAA GTC GCA GAG   54
                                     Met Glu Pro Lys Val Ala Glu
                                                            -45

CTG AAG CAG AAG ATC GAG GAC ACG CTA TGT CCT TTT GGC TTC GAG GTT   102
Leu Lys Gln Lys Ile Glu Asp Thr Leu Cys Pro Phe Gly Phe Glu Val
        -40   -35   -30

TAC CCC TTC CAG GTG GCA TGG TAC AAT GAA CTC TTG CCT CCA GCC TTC   150
Tyr Pro Phe Gln Val Ala Trp Tyr Asn Glu Leu Leu Pro Pro Ala Phe
    -25   -20   -15

CAC CTA CCG CTG CCA GGA CCT ACC CTG GCC TTC CTG GTA CTC AGC ACG   198
His Leu Pro Leu Pro Gly Pro Thr Leu Ala Phe Leu Val Leu Ser Thr
-10   -5   1   5

CCT GCC ATG TTT GAC CGG GCC CTC AAG CCC TTC TTG CAG AGC TGC CAC   246
Pro Ala Met Phe Asp Arg Ala Leu Lys Pro Phe Leu Gln Ser Cys His

```
                     10                      15                       20

CTC CGA ATG CTG ACT GAC CCA GTG GAC CAG TGT GTG GCC TAC CAT CTG      294
Leu Arg Met Leu Thr Asp Pro Val Asp Gln Cys Val Ala Tyr His Leu
        25                       30                   35

GGC CGT GTT AGA GAG AGC CTC CCA GAG CTG CAG ATA GAA ATC ATT GCT      342
Gly Arg Val Arg Glu Ser Leu Pro Glu Leu Gln Ile Glu Ile Ile Ala
        40                       45                   50

GRA HMA CGA GGT GCA CCC CAA CCG ACG CCC CAA GAT CCT GGC CCA GAC      390
Xaa Xaa Arg Gly Ala Pro Gln Pro Thr Pro Gln Asp Pro Gly Pro Asp
55                       60                   65                   70

AGC AGC CAT GTA GCT GGG GCT GCT                                      414
Ser Ser His Val Ala Gly Ala Ala
                75
```

(2) INFORMATION FOR SEQ ID NO: 192:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 400 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 324..389
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                     region 301..366
                                     id T08430
                                     est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 64..400
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 90
                                     region 1..337
                                     id C17891
                                     est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 301..400
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                     region 1..100
                                     id C04989
                                     est

```
(ix) .FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 107..145
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 3.7
                                seq MLVLRSGLTKALA/SR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:


AGAGTTCGCC AGTGGTCCAG GAGCCGCTTT TTTCCACTCG GGAAGACTTC AGAGAAGTCT    60

CACAAAGGAC TCGGCTGGCT GCTTTTCTCA GTGCCGAAGC CGCGCC ATG CTC GTT     115
                                                    Met Leu Val

CTC AGA AGC GGC CTG ACC AAG GCG CTT GCC TCA CGG ACG CTC GCG CCT    163
Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr Leu Ala Pro
-10              -5                  1               5

CAG GTG TGT TCA TCT TTT GCT ACG GGC CCT AGA CAA TAC GAT GGA ACG    211
Gln Val Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Thr
                10                  15                  20

TTC TAT GAA TTT CGT ACT TAT TAC CTT AAA CCT TCA AAT ATG AAT GCG    259
Phe Tyr Glu Phe Arg Thr Tyr Tyr Leu Lys Pro Ser Asn Met Asn Ala
        25                  30                  35

TTC ATG GAA AAT CTT AAG AAA AAC ATT CAT CTT CGG ACC TCT TAC TCT    307
Phe Met Glu Asn Leu Lys Lys Asn Ile His Leu Arg Thr Ser Tyr Ser
    40                  45                  50

GAA TTG GTT GGA TTC TGG AGT GTA GAA TTT GGA GGC AGA ACG AAT AAA    355
Glu Leu Val Gly Phe Trp Ser Val Glu Phe Gly Gly Arg Thr Asn Lys
55                  60                  65                  70

GTG TTT CAT ATT TGG AAG TAT GAT AAT TTT GCT CAT CGA GCT GAA        400
Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Ala Glu
                75                  80                  85
```

(2) INFORMATION FOR SEQ ID NO: 193:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 186 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 112..184
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 1..73
```

                                    id HSC09D101
                                    est

        (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 112..184
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 98
                                      region 1..73
                                      id HSC2UE011
                                      est

        (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 112..186
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 90
                                      region 1..75
                                      id HSC09C101
                                      est

        (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 140..184
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 95
                                      region 17..61
                                      id T35421
                                      est

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 106..174
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 10.5
                                      seq LLFVLLLFSLLPA/CL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ATATTTAAAC GACCCTTCAA AGGCCCTTAG GTTTCCTTGC CTCTGCTCAC AGAACTAGTC   60

CAGCCAGGTG TCGCTGCTGC CTCAGAGCTG TGTGGGGTCG CRTGT ATG TCG GGG GGC   117
                                                Met Ser Gly Gly
                                                            -20

CAT CTT GCC GAT TTA ACG CTG CTT TTT GTG TTG TTG TTG TTT TCC CTC   165
His Leu Ala Asp Leu Thr Leu Leu Phe Val Leu Leu Leu Phe Ser Leu
              -15   -10   -5

CTC CCT GCC TGC CTA CCC CGG   186
Leu Pro Ala Cys Leu Pro Arg
            1

(2) INFORMATION FOR SEQ ID NO: 194:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 335 base pairs
              (B) TYPE: NUCLEIC ACID

```
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

     (ii)  MOLECULE TYPE: CDNA

     (vi)  ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

     (ix)  FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(86..336)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 99
                                     region 79..329
                                     id AA148596
                                     est

     (ix)  FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(30..91)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 325..386
                                     id AA148596
                                     est

     (ix)  FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(2..39)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 92
                                     region 378..415
                                     id AA148596
                                     est

     (ix)  FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(2..336)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 99
                                     region 67..401
                                     id AA074631
                                     est

     (ix)  FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(83..336)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 99
                                     region 64..317
                                     id AA078818
                                     est

     (ix)  FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(8..48)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 97
                                     region 355..395
                                     id AA078818
```

```
                                        est

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(30..336)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 99
                                     region 64..370
                                     id N21054
                                     est

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(68..236)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 98
                                     region 172..340
                                     id AA157994
                                     est

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(225..336)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 94
                                     region 73..184
                                     id AA157994
                                     est

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(28..68)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 341..381
                                     id AA157994
                                     est

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 174..326
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 10.1
                                     seq LLGALTLLGLVTS/FY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:


AATTCTCAAC GAGCTGCGGG CTCGGCATGC CCAGGGGGGT ACATGGTATG GAGTAGACAT      60

CAACAACGAG GACATTGCTG ACAACTTTGA AGCTTTCGTG TGGGAGCCAG CTATGGTGCG     120

GATCAATGCG CTGACAGCAG CCTCTGAGGC TGCGTGCCTG ATCGTGTCTG TAG ATG       176
                                                            Met

AAA CCA TCA AGA ACC CCC GCT CGA CTG TGG ATG CTC CCA CAG CAG CAG      224
Lys Pro Ser Arg Thr Pro Ala Arg Leu Trp Met Leu Pro Gln Gln Gln
-50             -45             -40                     -35

GCC GGG GCC GTG GTC GTG GCC GCC CCC ACT GAG AGG CAC CCC ACC CAT      272
Ala Gly Ala Val Val Val Ala Ala Pro Thr Glu Arg His Pro Thr His
```

```
              -30                  -25                   -20
CAC ATG GCT GGC TGG CTG CTG GGT GCA CTT ACC CTC CTT GGC TTG GTT     320
His Met Ala Gly Trp Leu Leu Gly Ala Leu Thr Leu Leu Gly Leu Val
              -15                  -10                   -5

ACT TCA TTT TAC AAG                                                 335
Thr Ser Phe Tyr Lys
              1
```

(2) INFORMATION FOR SEQ ID NO: 195:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 419 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 23..200
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                            region 9..186
                            id W44639
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 216..356
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                            region 200..340
                            id W44639
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 363..412
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                            region 347..396
                            id W44639
                            est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 27..218
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 9.5
                            seq LSLLAALAHLAAA/EK

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
AGTGGGTCGA KCTGGGGCGC AGTCGC ATG GGG GAG.TCT ATC CCG CTG GCC GCC        53
                            Met Gly Glu Ser Ile Pro Leu Ala Ala
                                            -60

CCG GTC CCG GTG GAA CAG GCG GTG CTG GAG ACG TTC TTC TCT CAC CTG       101
Pro Val Pro Val Glu Gln Ala Val Leu Glu Thr Phe Phe Ser His Leu
-55             -50             -45             -40

GGT ATC TTC TCT TAC GAC AAG GCT AAG GAC AAT GTG GAG AAG GAA CGA       149
Gly Ile Phe Ser Tyr Asp Lys Ala Lys Asp Asn Val Glu Lys Glu Arg
            -35             -30             -25

GAG GCC AAC AAG AGC GCG GGG GGC AGC TGG CTG TCG CTG CTG GCG GCC       197
Glu Ala Asn Lys Ser Ala Gly Gly Ser Trp Leu Ser Leu Leu Ala Ala
            -20             -15             -10

TTG GCG CAC CTG GCC GCG GCC GAG AAG GTC TAT CAC AGC CTC ACC TAC       245
Leu Ala His Leu Ala Ala Ala Glu Lys Val Tyr His Ser Leu Thr Tyr
        -5              1               5

CTG GGG CAG AAA CTA GGG GGC CAG TCT TTC TTC AGC AGG AAG GAT TCC       293
Leu Gly Gln Lys Leu Gly Gly Gln Ser Phe Phe Ser Arg Lys Asp Ser
10              15              20              25

ATC CGC ACC ATC TAT ACT TCA TTG CAT AAT GAG CTG AAG AAG GTG GTG       341
Ile Arg Thr Ile Tyr Thr Ser Leu His Asn Glu Leu Lys Lys Val Val
            30              35              40

ACT GGC CGT GGT GCC DDK TNN TGG GAC TGC TCC TCA CGT GGA AGA ACT       389
Thr Gly Arg Gly Ala Xaa Xaa Trp Asp Cys Ser Ser Arg Gly Arg Thr
            45              50              55

CCT TTC CCA CCT GTC AGA GCA GCA TAC GGG                               419
Pro Phe Pro Pro Val Arg Ala Ala Tyr Gly
        60              65
```

(2) INFORMATION FOR SEQ ID NO: 196:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 342 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 33..269
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                              region 10..246
                              id AA058587

                                        est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 272..307
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 248..283
                                  id AA058587
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 133..259
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 87..213
                                  id R12128
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 47..134
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 2..89
                                  id R12128
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 303..337
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 97
                                  region 257..291
                                  id R12128
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 49..259
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 2..212
                                  id H19999
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 272..304
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 96
                                  region 225..257
                                  id H19999
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 303..337
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 91

```
                        region 257..291
                        id H19999
                        est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 42..252
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 99
                            region 1..211
                            id R20025
                            est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 87..259
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 99
                            region 1..173
                            id H83838
                            est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 272..337
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 98
                            region 186..251
                            id H83838
                            est
```

```
(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 85..198
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 9.3
                            seq QLLYLSLLSGLHG/QE
```

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:
```

```
AGGCTGCGGT AAATCCGGGC TTGCGGCCGC TGGCGTAGTC TGTGGCCGGG TGGTCGTTGC    60


TGCGCGCCCC GAGCCCCGAG AGCC ATG CAG ATG TCC TAC GCC ATC CGG TGC      111
                          Met Gln Met Ser Tyr Ala Ile Arg Cys
                          -35                        -30


GCC TTC TAC CAG CTG CTG CTG GCC GCG CTC ATG CTG GTG GCG ATG CTG     159
Ala Phe Tyr Gln Leu Leu Leu Ala Ala Leu Met Leu Val Ala Met Leu
              -25                 -20                 -15


CAG CTG CTC TAC CTG TCG CTG CTG TCC GGA CTG CAC GGG CAG GAG GAG     207
Gln Leu Leu Tyr Leu Ser Leu Leu Ser Gly Leu His Gly Gln Glu Glu
              -10                 -5                  1


CAA GAC CAA TAT TTT GAG TTC TTT CCC CCG TCC CCA CGG TCC GTG GAC     255
Gln Asp Gln Tyr Phe Glu Phe Phe Pro Pro Ser Pro Arg Ser Val Asp
    5                   10                  15


CAG GTC AAG GCT CAG CTC CGC ACC GCG CTG GCC TCT GGA GGC GTC CTG     303
Gln Val Lys Ala Gln Leu Arg Thr Ala Leu Ala Ser Gly Gly Val Leu
```

```
20              25              30              35

GAC GCT AGC GGC GAT TAC CGC GTC TAC AGG GGC CAT GGG          342
Asp Ala Ser Gly Asp Tyr Arg Val Tyr Arg Gly His Gly
              40              45
```

(2) INFORMATION FOR SEQ ID NO: 197:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 461 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(149..337)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                              region 182..370
                              id AA142966
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(340..459)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                              region 61..180
                              id AA142966
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(142..337)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                              region 183..378
                              id AA019334
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(340..459)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                              region 62..181
                              id AA019334
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(345..459)

        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                                region 48..162
                                id N66447
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(255..337)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                region 170..252
                                id N66447
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(111..181)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                                region 330..400
                                id N66447
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(179..228)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                                region 282..331
                                id N66447
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(172..337)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                region 113..278
                                id R85770
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(340..450)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                                region 1..111
                                id R85770
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 188..337
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                                region 1..150
                                id R78830
                                est

   (ix) FEATURE:

```
            (A) NAME/KEY: other
            (B) LOCATION: 339..459
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 96
                                    region 151..271
                                    id R78830
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 384..455
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 9.1
                                    seq LFAFHLLLSFILG/SR

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:
```

```
AACACTGTTG TATAAACTAA TCTTTGCTTG TTTTCTACTC TGTGATCTTT CCATATCATA    60

TTTCATTAAT GATCAGTTAG TGTCAAGGAG TCAAAACAGA TTAAAATTAA TTTCATGTGT   120

ATATGGTGGA AATTTGTGGC TAGTGTGATT TTTGTTTGTY TCCTTTTAAG TACTGTTGAT   180

CAGTTGTGAC ACTTACTGGT TAAACTTACG TTGCTAAAGA TTTCTCTATA ATAAGCCACA   240

CATTATATTT AGACTATATT AAGGGACCTT GGTTTCTTC TAGATAGCAG CTGTCCCAAA    300

GAAAATATTT CTTCTTTGTC TGTKAAGATT TAGCTATNKA TCTGCCAGTT GTTCAGMGGT   360

TTTGGTTCCA AACTCAACCA GCA ATG TTG AGA GCT GAA CTT AAG ATA GCT GTT  413
                         Met Leu Arg Ala Glu Leu Lys Ile Ala Val
                                     -20                     -15

GTA CTT TTT GCT TTC CAT CTG TTA CTG TCC TTC ATT CTC GGC TCC CGG    461
Val Leu Phe Ala Phe His Leu Leu Leu Ser Phe Ile Leu Gly Ser Arg
                  -10                     -5                  1
```

```
(2) INFORMATION FOR SEQ ID NO: 198:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 229 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

     (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(1..130)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 8..137
                                    id H63707
```

est

```
(ix)  FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 2..166
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 9
                              seq LLILLLRTFLCSA/MI

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 198:


A ATG AAT CAT CAA CAG ACA TTA ATT GGG CGC CTG CTC TGT GAT CTC CAT      49
  Met Asn His Gln Gln Thr Leu Ile Gly Arg Leu Leu Cys Asp Leu His
  -55             -50             -45             -40

GGG CTC AGC TTG TCC CCG CCA GTW GCC AAC AAC GTC CAA GCT CTC TTC        97
Gly Leu Ser Leu Ser Pro Pro Val Ala Asn Asn Val Gln Ala Leu Phe
            -35             -30             -25

AGA ATG CTT ACT CCT GAA GCT TAT TCC TGT CTT CTA ATT CTT TTG TTG      145
Arg Met Leu Thr Pro Glu Ala Tyr Ser Cys Leu Leu Ile Leu Leu Leu
        -20             -15             -10

AGG ACT TTT CTG TGT AGT GCA ATG ATA GCA AAT ACA CTT CAT CTC AAG      193
Arg Thr Phe Leu Cys Ser Ala Met Ile Ala Asn Thr Leu His Leu Lys
        -5               1               5

TAC CAT CTC CAA TTG ATT GAT AAT GCC TGC CCT GAG                       229
Tyr His Leu Gln Leu Ile Asp Asn Ala Cys Pro Glu
10               15              20
```


(2) INFORMATION FOR SEQ ID NO: 199:

```
      (i)  SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 278 base pairs
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: DOUBLE
           (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: other
           (B) LOCATION: 145..279
           (C) IDENTIFICATION METHOD: blastn
           (D) OTHER INFORMATION:  identity 100
                                   region 1..135
                                   id H06014
                                   est

      (ix) FEATURE:
           (A) NAME/KEY: other
           (B) LOCATION: 180..279
           (C) IDENTIFICATION METHOD: blastn
```

                        (D) OTHER INFORMATION: identity 100
                                                  region 11..110
                                                  id R15960
                                                  est

            (ix) FEATURE:
                    (A) NAME/KEY: other
                    (B) LOCATION: 204..279
                    (C) IDENTIFICATION METHOD: blastn
                    (D) OTHER INFORMATION: identity 96
                                             region 1..76
                                             id W67034
                                             est

            (ix) FEATURE:
                    (A) NAME/KEY: sig_peptide
                    (B) LOCATION: 27..146
                    (C) IDENTIFICATION METHOD: Von Heijne matrix
                    (D) OTHER INFORMATION: score 8.6
                                             seq LFCVLGIVLLVTG/IV

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

ACCAAACCAA AGCCGTCATC ATTGCA ATG ATC ATC ACT GCG GTG GTA TCC ATT   53
                                 Met Ile Ile Thr Ala Val Val Ser Ile
                                 -40   -35

TCA GTC ACC ATC TTC TGC TTT CAG ACC AAG GTG GAC TTC ACC TCG TGC   101
Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys
    -30   -25   -20

ACA GGC CTC TTC TGT GTC CTG GGA ATT GTG CTC CTG GTG ACT GGG ATT   149
Thr Gly Leu Phe Cys Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile
-15   -10   -5   1

GTC ACT AGC ATT GTG CTC TAC TTC CAA TAC GTT TAC TGG CTC CAC ATG   197
Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met
            5   10   15

CTC TAT GCT GCT CTG GGG GCC ATT TGT TTC ACC CTG TTC CTG GCT TAC   245
Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr
            20   25   30

GAC ACA CAG CTG GTC CTG GGG AAC CGG AAG CAC   278
Asp Thr Gln Leu Val Leu Gly Asn Arg Lys His
        35   40

(2) INFORMATION FOR SEQ ID NO: 200:

            (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 333 base pairs
                    (B) TYPE: NUCLEIC ACID
                    (C) STRANDEDNESS: DOUBLE
                    (D) TOPOLOGY: LINEAR

            (ii) MOLECULE TYPE: CDNA

            (vi) ORIGINAL SOURCE:

          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 55..268
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 95
                                  region 32..245
                                  id T60555
                                  est

      (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 22..51
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 90
                                  region 1..30
                                  id T60555
                                  est

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 67..261
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 8.4
                                  seq LLWFIHLVFVVLX/LF

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

AAGAGGCTTA CGAGSWCCAG GTGGAGAGGC CGGGCTGGCC AAGGCTTCGG CCTCCGGCGT   60

CGGGAA ATG GCG GCG GGG GGC AGG ATG GAG GAC GGT TCC TTG GAT ATC   108
       Met Ala Ala Gly Gly Arg Met Glu Asp Gly Ser Leu Asp Ile
       -65   -60   -55

ACC CAG AGT ATT GAA GAC GAC CCA CTT CTG GAT GCC CAG CTT CTC CCA   156
Thr Gln Ser Ile Glu Asp Asp Pro Leu Leu Asp Ala Gln Leu Leu Pro
-50   -45   -40

CAC CAC TCA TTA CAA GCT CAC TTT AGA CCC CGA TTC CAT CCT CTT CCT   204
His His Ser Leu Gln Ala His Phe Arg Pro Arg Phe His Pro Leu Pro
-35   -30   -25   -20

ACA GTC ATC ATA GTG AAT CTT CTG TGG TTT ATT CAT CTC GTG TTT GTT   252
Thr Val Ile Ile Val Asn Leu Leu Trp Phe Ile His Leu Val Phe Val
         -15   -10   -5

GTW TTA GSA TTG TTT AAC AGG TGT GCT TTG TTC TWA TCC TAT CCC AAA   300
Val Leu Xaa Leu Phe Asn Arg Cys Ala Leu Phe Xaa Ser Tyr Pro Lys
            1   5   10

TGG GAC ARG TGC CCA GGA AAT TAC ACA AAC CCA   333
Trp Asp Xaa Cys Pro Gly Asn Tyr Thr Asn Pro
    15   20

(2) INFORMATION FOR SEQ ID NO: 201:

```
(i)   SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 337 base pairs
      (B)  TYPE: NUCLEIC ACID
      (C)  STRANDEDNESS: DOUBLE
      (D)  TOPOLOGY: LINEAR

(ii)  MOLECULE TYPE: CDNA

(vi)  ORIGINAL SOURCE:
      (A)  ORGANISM: Homo Sapiens
      (F)  TISSUE TYPE: Brain

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 125..306
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 95
                               region 95..276
                               id H31193
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 69..130
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 93
                               region 40..101
                               id H31193
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: other
      (B)  LOCATION: 29..68
      (C)  IDENTIFICATION METHOD: blastn
      (D)  OTHER INFORMATION:  identity 97
                               region 1..40
                               id H31193
                               est

(ix)  FEATURE:
      (A)  NAME/KEY: sig_peptide
      (B)  LOCATION: 161..208
      (C)  IDENTIFICATION METHOD: Von Heijne matrix
      (D)  OTHER INFORMATION:  score 7.5
                               seq GCMLLFVFGFVGG/AV

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 201:


AATCGCTTGG GAGCTGCTGC AGGATGGAGT GGAAAGCTGC TGCTGATGGC ATTGTTTTTG      60

TGGCAGCAAG CTGAATGACA GATCCTCACT ACAAAGATAC CCCTTTGGCC CCCGTGTAGG     120

CCTCCTTGGT TCGGGTGTTT CACCATGCCA GCACAGCGCC ATG AGT CCT GGA TGC     175
                                             Met Ser Pro Gly Cys
                                                             -15

ATG CTG CTG TTT GTG TTT GGC TTT GTT GGC GGG GCG GTG GTC ATT AAT     223
Met Leu Leu Phe Val Phe Gly Phe Val Gly Gly Ala Val Val Ile Asn
    -10                 -5                  1                  5
```

```
TCT GCT ATC TTA GTA TCT CTC TCT GTT TTG CTG CTT GTG CAC TTT TCT    271
Ser Ala Ile Leu Val Ser Leu Ser Val Leu Leu Leu Val His Phe Ser
            10                  15                  20

ATT TCT ACC GGT GTG CCA GCT CTG ACG CAG AAC CTA CCA AGG ATA CTC    319
Ile Ser Thr Gly Val Pro Ala Leu Thr Gln Asn Leu Pro Arg Ile Leu
            25                  30                  35

AGA AAA GAA CGC CCC GGG                                            337
Arg Lys Glu Arg Pro Gly
            40
```

(2) INFORMATION FOR SEQ ID NO: 202:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 309 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 105..252
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                            region 136..283
                            id HSU46355
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 53..83
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 90
                            region 82..112
                            id HSU46355
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 227..276
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                            region 206..255
                            id AA011705
                            est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 109..153
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7.5
                            seq LLLGIALLAYVAS/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:


```
AATBGTGCAG CAGGCGGGCC CCCGCGCGGC AGGGSCCTGG ACCCGCGCGG CTCCCTGGGA    60

TGGTGAGCAA GGCGCTGCTG CSCTCGTGTC TGCCGTCAAC CGCAGASG ATG AAG CTG    117
                                                     Met Lys Leu
                                                     -15

CTG CTG GGC ATC GCC TTG CTG GCC TAC GTC GCC TCT GTT TGG GGC AAC    165
Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val Trp Gly Asn
        -10                 -5                   1

TTC GTT AAT ATG AGG TCT ATC CAG GAA AAT GGT GAA CTA AAA ATT GAA    213
Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu Lys Ile Glu
 5                 10                 15                 20

AGC AAG ATT GAA GAG ATG GTT GAA CCA CTA AGA GAG AAA ATC AGA GAT    261
Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys Ile Arg Asp
                25                 30                 35

TTA GRA AAA AGC TTT ACC CAG AAA TAC CCA CCA GTA AAG TTT TTA TCA    309
Leu Xaa Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys Phe Leu Ser
                40                 45                 50
```


(2) INFORMATION FOR SEQ ID NO: 203:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 491 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 132..251
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                                    region 170..289
                                      id T60981
                                      est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 19..126
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                                      region 57..164
                                      id T60981
                                      est

    (ix) FEATURE:

```
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 39..107
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 7.5
                                  seq LVLLLTLPLHLMA/LL

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:
```

```
AAGTGCCCCA GCGGAAGACA GCTCAGAGCT GGTCTGCC ATG GAC ATC CTG GTC CCA    56
                                           Met Asp Ile Leu Val Pro
                                                          -20

CTC CTG CAG CTG CTG GTG CTG CTT CTT ACC CTG CCC CTG CAC CTC ATG    104
Leu Leu Gln Leu Leu Val Leu Leu Leu Thr Leu Pro Leu His Leu Met
        -15                  -10                  -5

GCT CTG CTG GGC TGC TGG CAG CCC CTG TGC AAA AGC TAC TTC CCC TAC    152
Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys Lys Ser Tyr Phe Pro Tyr
  1           5                  10                  15

CTG ATG GCC GTG CTG ACT CCC AAG AGC AAC CGC AAG ATG GAG AGC AAG    200
Leu Met Ala Val Leu Thr Pro Lys Ser Asn Arg Lys Met Glu Ser Lys
            20                  25                  30

AAA CGG GAG CTC TTC AGC CAG ATA AAG GGG CTT ACA GGA GCC TCC GGG    248
Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly
            35                  40                  45

AAA GTG GCC CTA CTG GAG CTG GGC TGC GGA ACC GGA GCC AAC TTT CAG    296
Lys Val Ala Leu Leu Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln
        50                  55                  60

TTC TAC CCA CCG GGC TGC AGG GTC ACC TGC CTA GAC CCA AAT CCC CAC    344
Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His
        65                  70                  75

TTT GAG AAG TTC CTG ACA AAG AGC ATG GCT GAG AAC AGG CAC CTC CAA    392
Phe Glu Lys Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln
 80                  85                  90                  95

TAT GAG CGG TTT GTG GTG GCT CCT GGA GAG GAC ATG AGA MAG CTG GCT    440
Tyr Glu Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Xaa Leu Ala
                100                 105                 110

GAT GGC TCC ATG GAT GTK GTG GTC TGC ACT CTG GTG CTG TGC TCT GTG    488
Asp Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val
            115                 120                 125

CAG                                                                491
Gln
```

```
(2) INFORMATION FOR SEQ ID NO: 204:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 331 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR
```

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 25..303
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 98
                           region 1..279
                           id HSCOZA041
                           est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 131..286
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                           region 106..261
                           id R12615
                           est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 71..133
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 100
                           region 47..109
                           id R12615
                           est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 88..303
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 99
                           region 1..216
                           id HUM401H04B
                           est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 137..303
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 95
                           region 92..258
                           id T78771
                           est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 23..127
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 7.4
                           seq SLLLSLELASGSG/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```
AAAGGGCGGA STTCAGGTCT CC ATG GAG GCG GCT TCT CCT AGC AAC TCG ACG          52
                           Met Glu Ala Ala Ser Pro Ser Asn Ser Thr
                           -35                     -30

GGC GTT GAG CGG ASC GCT GAC CTG ATG GAC GCC GAC AGC CTC CTG CTG          100
Gly Val Glu Arg Xaa Ala Asp Leu Met Asp Ala Asp Ser Leu Leu Leu
-25             -20             -15                     -10

TCT CTG GAG CTG GCG TCC GGC AGT GGG CAG GGC CTC AGC CCG GAC CGT          148
Ser Leu Glu Leu Ala Ser Gly Ser Gly Gln Gly Leu Ser Pro Asp Arg
                -5               1              5

CGG GCC TCG CTG CTC ACG TCT CTT ATG CTG GTT AAG CGC GAC TAC CGC          196
Arg Ala Ser Leu Leu Thr Ser Leu Met Leu Val Lys Arg Asp Tyr Arg
            10              15              20

TAT GAT CGG GTT CTC TTC TGG GGC CGC ATC CTT GGC CTC GTC GCC GAT          244
Tyr Asp Arg Val Leu Phe Trp Gly Arg Ile Leu Gly Leu Val Ala Asp
        25              30              35

TAC TAC ATC GCG CAG GGC CTG AGT GAG GAC CAG CTC GCA CCG CGC AAG          292
Tyr Tyr Ile Ala Gln Gly Leu Ser Glu Asp Gln Leu Ala Pro Arg Lys
40              45              50              55

ACG CTC TAT AGG TCC AGA TCA AGG AAG AGA CCC GCA CTG                      331
Thr Leu Tyr Arg Ser Arg Ser Arg Lys Arg Pro Ala Leu
            60              65
```

(2) INFORMATION FOR SEQ ID NO: 205:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 317 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 46..119
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 93
                                      region 12..85
                                      id N80832
                                      est

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 88..119
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 100
                                      region 1..32
                                      id H92328

est

(ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 108..236
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7.4
                                seq VLVKLLSSSASTS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

AGTTTCGNST CGCGGATCCG GTAGGTCCAG GTGCAGCGGC CGCAGTKCTG CGTCCGTGCG   60

CCGCGGGCTG GGGCGGTCTC AGGTGTGCCG AAGCTCTGGT CAGTGCC ATG ATC CGG   116
                                                    Met Ile Arg

CAG GAG CGC TCC ACA TCC TAC CAG GAG GCT GTG CGT CCA GCG CTT CCT   164
Gln Glu Arg Ser Thr Ser Tyr Gln Glu Ala Val Arg Pro Ala Leu Pro
-40   -35   -30   -25

TCA AGC AAG CCC TGC CTC CTC ACT TCT CCA GCT GTA TTA GTG AAA CTG   212
Ser Ser Lys Pro Cys Leu Leu Thr Ser Pro Ala Val Leu Val Lys Leu
        -20   -15   -10

CTC TCC TCC TCC GCC TCC ACT TCT CGG CCC CCA GAC CTT GGT CAT CTT   260
Leu Ser Ser Ser Ala Ser Thr Ser Arg Pro Pro Asp Leu Gly His Leu
        -5   1   5

TGG CAA CCG TCC TCT TCT GTG CCC CTC CAT CGG CCG CCA CAC ACT GCA   308
Trp Gln Pro Ser Ser Ser Val Pro Leu His Arg Pro Pro His Thr Ala
    10   15   20

CCA CCA GCG   317
Pro Pro Ala
 25

(2) INFORMATION FOR SEQ ID NO: 206:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 363 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 26..365
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 96
                                region 1..340
                                id M40260
                                est

189

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 17..308
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 93
                            region 6..297
                            id W07706
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 311..349
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 100
                            region 301..339
                            id W07706
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 79..365
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 95
                            region 22..308
                            id W37568
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 140..326
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 93
                            region 74..260
                            id W00732
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 328..365
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 100
                            region 263..300
                            id W00732
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 79..362
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 95
                            region 14..297
                            id AA135041
                            est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 25..147
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 7.4
                            seq ILPLLFGCLGVFG/LF
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
ACACGTCACT TCCGAGGCGG GAGG ATG AAG TTG ATT GAC TAT GGT CTC TCC        51
                            Met Lys Leu Ile Asp Tyr Gly Leu Ser
                            -40                 -35

GGC TAC CAG GAA GAG TCT GCC GAA GTG AAG GCC ATG GAC TTC ATC ACC        99
Gly Tyr Gln Glu Glu Ser Ala Glu Val Lys Ala Met Asp Phe Ile Thr
        -30             -25             -20

TCC ACA GCC ATC CTG CCC CTG CTG TTC GGC TGC CTG GGC GTC TTC GGC       147
Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys Leu Gly Val Phe Gly
    -15             -10             -5

CTC TTC CGG CTG CTG CAG TGG GTG CGC GGG AAG GCC TAC CTG CGG AAT       195
Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys Ala Tyr Leu Arg Asn
1           5               10              15

GCT GTG GTG GTG ATC ACA GGC GCC ACC TCA GGG CTG GGC AAA GAA TGT       243
Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly Leu Gly Lys Glu Cys
        20              25              30

GCA AAA GTC TTC TAT GCT RMG GGT GCT AAA CTG GTG CTC TGT GAR MCG       291
Ala Lys Val Phe Tyr Ala Xaa Gly Ala Lys Leu Val Leu Cys Glu Xaa
        35              40              45

GAA TGG TGG GGC CTA GAA GAG CTC ATC AGA GAA CTC ACC GCT TCT CAT       339
Glu Trp Trp Gly Leu Glu Glu Leu Ile Arg Glu Leu Thr Ala Ser His
    50              55              60

GCC ACC AAG GTG CAG ACA CAC AAG                                       363
Ala Thr Lys Val Gln Thr His Lys
65              70
```

(2) INFORMATION FOR SEQ ID NO: 207:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 235 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 60..181
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                       region 1..122
                       id AA057454
                       est

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 182..233
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 96
                             region 122..173
                             id AA057454
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 71..233
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 99
                             region 1..163
                             id C18312
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 182..233
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 144..195
                             id W69247
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 98..144
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 62..108
                             id W69247
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 34..78
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 1..45
                             id W69247
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 146..233
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 69..156
                             id H75891
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 76..144
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 95
                             region 1..69
                             id H75891
```

est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 80..233
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 98
                            region 1..154
                            id HUML11265
                            est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 104..160
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 7.4
                            seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

ATAAGGGGGA ACCCGCTGGC CCAATGGCAG CGTCCTACAG TGTAGCCTCC GCCTCCCGAT   60

TGACTGGCCT GCTTGGCAAK GCAAGTAGCG GCGGCGCTTC AAG ATG CGC TGC CTG   115
                                                Met Arg Cys Leu

ACC ACG CCT ATG CTG CTG CGG GCC CTG GCC CAG GCT GCA CGT GCA GGA   163
Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala Ala Arg Ala Gly
-15   -10   -5   1

CCT CCT GGT GGC CGG AGC CTC CAC AGC AGT GCA GTG GCA GCC ACC TAC   211
Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val Ala Ala Thr Tyr
            5   10   15

AAG TAT GTG AAC ATG CAG GAT CAA   235
Lys Tyr Val Asn Met Gln Asp Gln
        20   25

(2) INFORMATION FOR SEQ ID NO: 208:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 385 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 70..351
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                region 34..315
                                id T19063

```
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 36..68
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 96
                             region 1..33
                             id T19063
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 61..353
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                             region 1..293
                             id T32338
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 93..360
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 99
                             region 1..268
                             id T30463
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(107..265)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 91
                             region 330..488
                             id W27204
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(257..385)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 99
                             region 209..337
                             id W27204
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 70..324
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 99
                             region 27..281
                             id T32187
                             est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 134..334
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 7
```

seq IWTLLSSVIRCLC/AI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

AGACAAATGG CTCAGGTGGA CTCCGGGCTG GAGCTGTCCT GGGGGAGCTT GTTTGCGGCA   60

SGGCTGCTGC TGCCACTGCT GTGCTGGSGG CCCGGTCGCC AGGCAAAAAG CCCTCCCACG   120

TTTGAGGGGA GTC ATG AGC CGT TTC CTG AAT GTG TTA AGA AGT TGG CTG   169
            Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu
               -65   -60

GTT ATG GTG TCC ATC ATA GCC ATG GGG AAC ACG CTG CAG AGC TTC CGA   217
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg
-55   -50   -45   -40

GAC CAC ACT TTT CTC TAT GAA AAG CTC TAC ACT GGC AAG CCA AAC CTT   265
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu
            -35   -30   -25

GTG AAT GGC CTC CAA GCT CGG ACC TTT GGG ATC TGG ACG CTG CTC TCA   313
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser
        -20   -15   -10

TCA GTG ATT CGC TGC CTC TGT GCC ATT GAC ATT CAC AAC AAG ACG CTC   361
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu
        -5   1   5

TAT CAC ATC ACA CTC TGG ACC TTC   385
Tyr His Ile Thr Leu Trp Thr Phe
 10   15

(2) INFORMATION FOR SEQ ID NO: 209:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 285 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(2..55)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 92
                                     region 34..87
                                     id T86932
                                     est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(45..86)

```
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 2..43
                                id T86932
                                est


    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 199..240
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 6.8
                                seq IFLTLSLDSRVSA/IR


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:


AAATAAAAAT ATCTTAAAAC TGCATTGTAC AGCTCCCTCC CTGCGTTTTA TTAAATGATG    60

TATATTAAAC AAAGATCAAT ATTTTCTTAA TGACTCAGGG TCTTTATTGT TAATGCCAAT   120

TGTTTTTGTA TCTGTGCTAT AATCCCTTAG AGTCAGTAAA GTATGTAGGG GACTGTTTCT   180

TCCTTTGTGT CTGGGTTT ATG ATT TTT CTC ACT CTT TCT TTG GAC TCC AGG     231
                    Met Ile Phe Leu Thr Leu Ser Leu Asp Ser Arg
                                        -10                 -5

GTG TCA GCC ATC AGG TCT CCT AAT TTT GTG TAC CGG TCT CCA ACA DMC     279
Val Ser Ala Ile Arg Ser Pro Asn Phe Val Tyr Arg Ser Pro Thr Xaa
        1               5                       10

CAT GGG                                                             285
His Gly
    15



(2) INFORMATION FOR SEQ ID NO: 210:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 378 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 65..270
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 109..314
                                id AA100852
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
```

```
        (B) LOCATION: 269..378
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 94
                                region 314..423
                                id AA100852
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 65..270
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 109..314
                                id AA161042
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 277..361
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 94
                                region 323..407
                                id AA161042
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 65..274
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 104..313
                                id H64488
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 68..256
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 147..335
                                id AA146605
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 256..317
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 336..397
                                id AA146605
                                est

(ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 80..305
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 129..354
                                id AA088770
                                est
```

```
(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 76..162
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 6.8
                             seq LIFLCGAALLXVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:
```

```
AATACTACAC ACTCATATAG GGGAGGGAGG CTTCTGGGTC CCAGGGCCGC AGGGGCAKKG   60


AAGTCTGGAG CCWYC ATG CAG TGC TTC AGC TTC ATT AAG ACC ATG ATG ATC   111
                Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile
                    -25                     -20

CTC TTC AAT TTG CTC ATC TTT CTG TGT GGT GCA GCC CTG TTR RCA GTG   159
Leu Phe Asn Leu Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Xaa Val
    -15               -10                     -5

GGC ATC TGG GTG TCA ATC GAT GGG GCA TCC TTT CTG AAG ATC TTC GGG   207
Gly Ile Trp Val Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly
1               5                   10                      15

CCA CTG TCG TCC AGT GCC ATG CAG TTT GTC AAC GTG GGC TAC TTC CTC   255
Pro Leu Ser Ser Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu
            20              25                  30

ATC GCA GCC GGC GTT GTG GTC TTT GCT CTY GGT TTC CTG GGC TGC TAT   303
Ile Ala Ala Gly Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr
            35              40                  45

SGT GCT AAG ACT GAG AGC WAG TGT GCC CTC GTG ACG TTC TTC TKC ATC   351
Xaa Ala Lys Thr Glu Ser Xaa Cys Ala Leu Val Thr Phe Phe Xaa Ile
        50              55                  60

CTC CTS CTC ATC TTC ATT GCT GAC GTT                               378
Leu Leu Leu Ile Phe Ile Ala Asp Val
65                  70
```

```
(2) INFORMATION FOR SEQ ID NO: 211:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 327 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 234..288
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 96
```

region 203..257
id R25833
est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 285..317
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                              region 255..287
                              id R25833
                              est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 37..141
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.4
                              seq SACLLLCPTWTNP/QL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:


```
AAAAAAGGCG GGGTCTCGGC CGGCGCTGAC GCAGCC ATG GCG GAG GCG GCT TTG        54
                                        Met Ala Glu Ala Ala Leu
                                        -35                  -30

GAA GCC GTG CGG ASG AGT TAC GAG AAT TCC CGG CCG CTG CAA GGG AGC       102
Glu Ala Val Arg Xaa Ser Tyr Glu Asn Ser Arg Pro Leu Gln Gly Ser
            -25             -20             -15

TCT GCG TGC CTC TTG CTG TGC CCT ACC TGG ACA AAC CCC CAA CTC CGC       150
Ser Ala Cys Leu Leu Leu Cys Pro Thr Trp Thr Asn Pro Gln Leu Arg
        -10             -5                      1

TCC ACT TCT ACC GGG ACT GGG TCT GCC CCA ACA GGC CGT GCA TTA TCC       198
Ser Thr Ser Thr Gly Thr Gly Ser Ala Pro Thr Gly Arg Ala Leu Ser
 5               10               15

GCA ACG CTC TGC AGC ACT GGC CGG CCC TCC ANC DKK TGG TCC CTC CCC       246
Ala Thr Leu Cys Ser Thr Gly Arg Pro Ser Xaa Xaa Trp Ser Leu Pro
 20               25               30                       35

TAT TTC AGA GCC ACA GTG GGC TCC ACA GAG GTG AGT GTG GCC GTG ACC       294
Tyr Phe Arg Ala Thr Val Gly Ser Thr Glu Val Ser Val Ala Val Thr
             40               45               50

CCA GAT GGT TAC GCG GAT GCC GTD AGA NGG GAT                           327
Pro Asp Gly Tyr Ala Asp Ala Val Arg Xaa Asp
         55               60
```

(2) INFORMATION FOR SEQ ID NO: 212:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 244 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 82..241
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 99
                            region 51..210
                            id C18780
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 48..83
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 94
                            region 18..53
                            id C18780
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 163..235
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                            region 121..193
                            id T11911
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 116..162
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 95
                            region 73..119
                            id T11911
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 204..239
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 94
                            region 226..261
                            id T69629
                            est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 143..199
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 6.4
                            seq SVFLLMVNGQVES/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AGCACTCGCG TGGCCTTCGC GAAGGTGTCG CTGCCAAGAA ACGTGTCCTG CGCGCTACGC   60

CGTCTGTTTT TAGGGCAACG CCGGCGTCTC TTAGCAACCG CGCGCGGCCT AGGTGGGTCC   120

CCCCGGCACC CCCAGACCTG CC ATG GCG ACC GCG AGT CCT AGC GTC TTT CTA   172
                         Met Ala Thr Ala Ser Pro Ser Val Phe Leu
                                         -15   -10

CTC ATG GTC AAC GGG CAG GTG GAG AGC GCC CAG TTT CCA GAG TAT GAT   220
Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp
             -5   1   5

GAC CTC TAC TGC AAG TAC TGC CAG   244
Asp Leu Tyr Cys Lys Tyr Cys Gln
         10   15

(2) INFORMATION FOR SEQ ID NO: 213:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 211 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 95..208
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 100
                                    region 85..198
                                    id N43024
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 28..95
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 91
                                    region 17..84
                                    id N43024
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 107..199
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                    region 80..172
                                    id T62095
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other

          (B) LOCATION: 61..106
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 93
                                  region 35..80
                                  id T62095
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 26..60
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 97
                                  region 1..35
                                  id T62095
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 61..208
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 26..173
                                  id W42796
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 110..208
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 92
                                  region 114..212
                                  id AA030227
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 110..208
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 92
                                  region 51..149
                                  id AA118270
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 104..187
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 6
                                  seq IGLMFLMLGCALP/IY

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TCTTCCGGGT GTTGTCTGGC CGCCGTAGCG CRTCTTGGGT CTCCCGGCTG CCGCTGCTGC   60

CGCCGCCGCC TCGGGTCGTG CAGCCAGGAG CGACGTCACC GCC ATG GCA GGC ATC   115
                                            Met Ala Gly Ile
                                                         -25

AAA GCT TTG ATT AGT TTG TCC TTT GGA GGA GCA ATC GGA CTG ATG TTT   163
Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe

```
        .      -20                 -15                 -10
TTG ATG CTT GGA TGT GCC CTT CCA ATA TAC AAC AAA TAC TGG CCC TGG      211
Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Trp
            -5                  1                   5
```

(2) INFORMATION FOR SEQ ID NO: 214:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 3..124
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                           region 8..129
                           id AA146587
                           est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 2..124
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                           region 14..136
                           id T85006
                           est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 11..124
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                           region 1..114
                           id H08511
                           est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 14..124
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                           region 1..111
                           id C00740
                           est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 13..124

```
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 1..112
                                    id N40664
                                    est


       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 12..62
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.9
                                    seq ILLFGTLLMNAGA/VL


       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:


AGGCCGTAAC G ATG ATC GGA GAC ATC CTG CTG TTC GGG ACG TTG CTG ATG      50
             Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met
                 -15                 -10                     -5

AAT GCC GGG GCG GTG CTG AAC TTT AAG CTG AAA AAG AAG GAC ACG CAG       98
Asn Ala Gly Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln
                 1               5               10

GGC TTT GGG GAG GAG TCC AGG GAG CCT TGG                              128
Gly Phe Gly Glu Glu Ser Arg Glu Pro Trp
        15              20



(2) INFORMATION FOR SEQ ID NO: 215:


       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 150 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR


      (ii) MOLECULE TYPE: CDNA


      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain


      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 12..143
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 99
                                    region 36..167
                                    id HUM137D01B
                                    est


      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 12..142
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 99
                                    region 143..273
                                    id AA155928
                                    est
```

```
    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 12..141
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 99
                                  region 115..244
                                  id W39572
                                  est


    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(12..135)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 95
                                  region 1..124
                                  id M78698
                                  est


    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(32..151)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 98
                                  region 346..465
                                  id H99266
                                  est


    (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 67..114
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 5.9
                                  seq MILTLSLFGSCIS/NF


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:


ACACATCCCT CTAAACTACT GTTAGGAACA GCAGTGTTCT CACAGTGTRG GGCAGCCGTC    60

CTTCTA ATG AAG ACA ATG ATA TTG ACA CTG TCC CTC TTT GGC AGT TGC     108
       Met Lys Thr Met Ile Leu Thr Leu Ser Leu Phe Gly Ser Cys
       -15             -10                 -5

ATT AGT AAC TTT GAA AGG TAT ATG ACT GAG CGT AGC ATC CAG            150
Ile Ser Asn Phe Glu Arg Tyr Met Thr Glu Arg Ser Ile Gln
     1           5                 10
```

```
(2) INFORMATION FOR SEQ ID NO: 216:

    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 397 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
```

```
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(223..398)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:   identity 96
                                     region 111..286
                                     id HSGT545
                                     est

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(69..219)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:   identity 92
                                     region 291..441
                                     id HSGT545
                                     est

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(2..43)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:   identity 97
                                     region 467..508
                                     id HSGT545
                                     est

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(223..311)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:   identity 92
                                     region 4..92
                                     id AA036134
                                     est

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(46..163)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:   identity 91
                                     region 133..250
                                     id AA038839
                                     est

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(223..295)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:   identity 97
                                     region 1..73
                                     id AA038839
                                     est

     (ix)  FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 326..387
            (C) IDENTIFICATION METHOD: blastn
```

        (D) OTHER INFORMATION: identity 91
                                 region 2..63
                                 id W51392
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 152..268
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.9
                                 seq SVSVLSSLGIVLA/VV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

ACTTTGAGGG TGTCTCTGGC CATGTGGTGT TTGATGCCAG CBGCTCTCGG ATGGCATGGA   60

CGCTTATCGA GCAGCTTCAG GGTGGCAGCT ACAAGAAGAT TGGCTACTAT GACAGCACCA   120

AGGATGATCT TTCCTGGTCC AAAACAGATA A ATG GAT TGG AGG GTC CCC CCC   172
                                  Met Asp Trp Arg Val Pro Pro
                                                     -35

AGC TGR SCA GAC CCT GGT CAT CAA GAC ATT CCG CTT CCT GTC ACA GAN   220
Ser Xaa Xaa Asp Pro Gly His Gln Asp Ile Pro Leu Pro Val Thr Xaa
        -30   -25   -20

NNC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTC CTA GCT   268
Xaa Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
    -15   -10   -5

GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC CGT TAT ATC   316
Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
 1   5   10   15

CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG GGC TGC TCA   364
Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
            20   25   30

MTG GCT TTA GCT GCT GTC TTC CCC TGG GGC TCG   397
Xaa Ala Leu Ala Ala Val Phe Pro Trp Gly Ser
        35   40

(2) INFORMATION FOR SEQ ID NO: 217:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 373 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other

        (B) LOCATION: 41..337
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                                 region 1..297
                                 id H56523
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 38..337
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                 region 1..300
                                 id AA020823
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 43..337
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                 region 7..301
                                 id H99096
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 49..315
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                                 region 11..277
                                 id AA083141
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 52..337
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                 region 17..302
                                 id N21197
                                 est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 35..82
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.8
                                 seq AALPAWLSLQSRA/RT

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGCTTGTCCC CTCCGGCTTG CCGTCCTCGC AGCC ATG GCG GCC GCC GCG CTC CCA   55
                                      Met Ala Ala Ala Ala Leu Pro
                                      -15   -10

GCA TGG CTG TCT CTG CAG TCG AGG GCA AGG ACT CTG CGT GCA TTC TCC   103
Ala Trp Leu Ser Leu Gln Ser Arg Ala Arg Thr Leu Arg Ala Phe Ser
          -5   1   5

```
ACT GCC GTC TAC TCG GCC ACT CCG GTC CCG ASA CCT AGC CTG CCG GAA        151
Thr Ala Val Tyr Ser Ala Thr Pro Val Pro Xaa Pro Ser Leu Pro Glu
        10                  15                  20

AGA ACA CCC GGA AAT GAA AGG CCA CCA AGA AGA AAG GCA CTA CCT CCT        199
Arg Thr Pro Gly Asn Glu Arg Pro Pro Arg Arg Lys Ala Leu Pro Pro
    25                  30                  35

AGG ACA GAG AAA ATG GCT GTT GAC CAG GAC TGG CCT AKT GTT TAC CCA        247
Arg Thr Glu Lys Met Ala Val Asp Gln Asp Trp Pro Xaa Val Tyr Pro
    40                  45                  50                  55

GTT GCA GCA CCA TTT AAA CCC TCT GCA GTA CCT CTT CCT GTT CGA ATG        295
Val Ala Ala Pro Phe Lys Pro Ser Ala Val Pro Leu Pro Val Arg Met
                60                  65                  70

GGT TAT CCA GTA AAA AAG GGC GTS CCA TGG SAA AGG AGG GAA TCT AKG        343
Gly Tyr Pro Val Lys Lys Gly Val Pro Trp Xaa Arg Arg Glu Ser Xaa
                75                  80                  85

ACT TTT AAA GAT TCC AAT TTT CTG CAT TTG                                373
Thr Phe Lys Asp Ser Asn Phe Leu His Leu
        90                  95
```

(2) INFORMATION FOR SEQ ID NO: 218:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 333 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 32..331
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                                region 1..300
                                id R13004
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 114..274
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                                region 54..214
                                id T80337
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 272..331

```
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 213..272
                                     id T80337
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 66..106
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 6..46
                                     id T80337
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 101..278
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 94
                                     region 70..247
                                     id T08840
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 33..113
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 98
                                     region 1..81
                                     id T08840
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 101..249
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 95
                                     region 72..220
                                     id HSCOCF041
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 31..112
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 1..82
                                     id HSCOCF041
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 247..321
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 5.8
                                     seq LWISACAMLLCHG/SL

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:
```

AAGCTAGGAC ATTCTTCTCC TCCTGGCCCT GGACATCAGA ACCCCAGGCT CTCCAGCCTT   60

TGGACTTCAG GACTGACACA AGCAACCTGC TGGGTTCTTA GGCCTTTGGC TTGTACTGAG   120

ACTTACACCA TCAGCTTCCC TGGTCCTGAG ACTTTTGGAC TTGGATTGAG CCACGCTACT   180

GGCATCCCAG GATCTCCAGC TTGCAGACAG CCTGTCGTGG GACTTCACAG CCTCCATAAT   240

TATAGA ATG GCA ATG GTC TCT GCG ATG TCC TGG GTC CTG TAT TTG TGG   288
       Met Ala Met Val Ser Ala Met Ser Trp Val Leu Tyr Leu Trp
       -25   -20   -15

ATA AGT GCT TGT GCA ATG CTA CTC TGC CAT GGA TCC CTT CAG CGG   333
Ile Ser Ala Cys Ala Met Leu Leu Cys His Gly Ser Leu Gln Arg
-10   -5   1

(2) INFORMATION FOR SEQ ID NO: 219:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 284 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(2..282)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 100
                                    region 59..339
                                    id H10776
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(64..282)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 96
                                    region 73..291
                                    id N94455
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(2..85)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                    region 271..354
                                    id N94455
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other

```
              (B) LOCATION: complement(107..282)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:   identity 99
                                       region 58..233
                                       id H64097
                                       est

     (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: complement(2..120)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:   identity 94
                                       region 219..337
                                       id H64097
                                       est

     (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: complement(38..282)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:   identity 99
                                       region 60..304
                                       id R98226
                                       est

     (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: complement(161..282)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:   identity 96
                                       region 33..154
                                       id W60134
                                       est

     (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: complement(9..120)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:   identity 96
                                       region 195..306
                                       id W60134
                                       est

     (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 51..257
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:   score 5.7
                                       seq LCRLLCLVRLFCC/SS

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:


ATCAACCATC CAGCTCCCAG CTGGCTAAAC TTTGCCTCCA GTGGTCAAAG ATG GGA      56
                                                          Met Gly


AAA GAG TGG GGT TGG CAG GAG ATG GAA AAC GGA GGT GCC GCC CCA GCA    104
Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala Pro Ala
      -65                  -60                  -55


TGG GGG GCA GGT CCC CCA GTC CAC CCT GCC CCT CCC CCT GTG GAG AAG    152
```

Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val Glu Lys
   -50   -45   -40

ACG CTT AGT TGG GGG TGT GGG TTT GGG CTC CAT TCT GGA TTC GGC GGT   200
Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe Gly Gly
-35   -30   -25   -20

TCC GGG GGA GGG GTG GGT CTG TGC CGA TTA CTC TGT CTT GTA CGT TTG   248
Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val Arg Leu
                -15   -10   -5

TTC TGC TGC TCT TCA ATA TTG TAT CAA CGC CAG GGG   284
Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Gly
          1   5

(2) INFORMATION FOR SEQ ID NO: 220:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 361 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 137..358
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 97
                                     region 151..372
                                     id N33828
                                     est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 2..124
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                     region 14..136
                                     id N33828
                                     est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 138..358
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                     region 147..367
                                     id N34173
                                     est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 1..148

```
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 11..158
                                    id N34173
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 35..358
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 99
                                    region 1..324
                                    id T89546
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 138..337
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 107..306
                                    id H67305
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 42..148
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 99
                                    region 12..118
                                    id H67305
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 138..302
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 112..276
                                    id T79378
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 33..145
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 100
                                    region 8..120
                                    id T79378
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 317..348
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 100
                                    region 293..324
                                    id T79378
                                    est

    (ix) FEATURE:
```

            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 167..229
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.6
                                    seq LVLSLQFLLLSYD/LF

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

AATGACAACC GACGTTGGAG TTTGGAGGTG CTTGCCTTAG AGCAAGGGAA ACAGCTCTCA   60

TTCAAAGGAA CTAGAAGCCT CTCCCTCAGT GGTAGGGAGA CAGCCAGGAG CGGTTTTCTG   120

GGAACTGTGG GATGTGCCCT TGGGGGCCCG AGAAACAGA AGGAAG ATG CTC CAG   175
                                                    Met Leu Gln
                                                        -20

ACC AGT AAC TAC AGC CTG GTG CTC TCT CTG CAG TTC CTG CTG CTG TCC   223
Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu Leu Leu Ser
        -15   -10   -5

TAT GAC CTC TTT GTC AAT TCC TTC TCA GAA CTG CTC CAA AAG ACT CCT   271
Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro
         1   5   10

GTC ATC CAG CTT GTG CTC TTC ATC ATC CAG GAT ATT GCA GTC CTC TTC   319
Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala Val Leu Phe
 15   20   25   30

AAC ATC ATC ATC ATT TTC CTC ATG TTC TTC AAC ACC TCC CGG   361
Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser Arg
             35   40

(2) INFORMATION FOR SEQ ID NO: 221:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 252 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(100..250)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                    region 256..406
                                    id W72958
                                    est

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 115..250

```
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 99
                                    region 2..137
                                    id W78821
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 120..250
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 99
                                    region 1..131
                                    id AA083784
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 115..250
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 4..139
                                    id W24219
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 145..250
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 97
                                    region 39..144
                                    id C15963
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 114..153
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 95
                                    region 9..48
                                    id C15963
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 172..243
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.5
                                    seq MGVCLLIPGLATA/CI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:


AGCGCGASGY CCGKCTCTCT TGTGCCCTAG CAGATTCCGT CGCTTCTTCC GGAGCCGTAC    60

GTGGTACCGC CCCGCTCGCG GGCGGCCGCG RGGCTTGCTG GGAAGAGAGG CGAACCAGGT   120

CACCTTTCAA GGACCCAGAA GTAGGGTTTT GGCCTAGGTA ACGGGGCAGA G ATG TGG   177
                                                            Met Trp

TTC GAG ATT CTC CCC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT   225
Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile
```

             -20   -15   -10

CCA GGA CTG GCT ACT GCG TGC ATC CGG   252
Pro Gly Leu Ala Thr Ala Cys Ile Arg
     -5   1

(2) INFORMATION FOR SEQ ID NO: 222:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 167 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(2..103)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                    region 48..149
                                    id AA126155
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(98..143)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                    region 7..52
                                    id AA126155
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 30..95
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.5
                                    seq LADPLXLFPFSEG/LP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

ACTGCTCSTG GAGCTCTGCG CTGGTCTTC ATG CGC CCT AGC CCT CTT TCG GGG   53
                                   Met Arg Pro Ser Pro Leu Ser Gly
                                   -20   -15

ATA CTG GCC GAC CCC CTC TKC CTT TTC CCC TTT AGT GAA GGC CTC CCC   101
Ile Leu Ala Asp Pro Leu Xaa Leu Phe Pro Phe Ser Glu Gly Leu Pro
              -10   -5   1

CGT CGC CGC GCG GCT TCC CGG AGC CGA CTG CAG ACT CCC TCA GCC CGG   149
Arg Arg Arg Ala Ala Ser Arg Ser Arg Leu Gln Thr Pro Ser Ala Arg
             5   10   15

TGT TCC CCG CGT CCG GGG   167
Cys Ser Pro Arg Pro Gly
      20

(2) INFORMATION FOR SEQ ID NO: 223:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 350 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 40..352
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 30..342
                                id H15315
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 12..46
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 91
                                region 1..35
                                id H15315
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 77..300
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                                region 1..224
                                id HUM427H08B
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 22..134
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 91
                                region 3..115
                                id AA071651
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 138..326
        (C) IDENTIFICATION METHOD: blastn

          . (D) OTHER INFORMATION: identity 95
                                     region 32..220
                                     id R35596
                                     est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 65..111
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 91
                                   region 1..47
                                   id W55530
                                   est

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 261..341
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 5.4
                                   seq SLMMAQXFIPAVA/KV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AGGAGGGCTG GACAGCAGCT CAGCTCGCTA GCTGCGCGCT TCCCGGCACA GGCAGTGCCA   60

CTGCGCAGGT TGATCAGCGA AACAGCATCC ATTTTAATCT GCGGGGAGNN CCTGCCTTAC   120

CAGGGCGTTC TCTCCGCCCG CCGGTGGATG CTCCGCGCCT GCSCTCCGCA GCCTCGCTCA   180

GCAGTCCTGC GTTGGGGTCT GCGCCCTAGG ATGCACTGAG ATGGTACATC AGGATAACTG   240

CTCGTATCAG GCACAGAAAA ATG AGA GAG AGT CTA TCA DKS AGA AGT TGG CAC   293
                      Met Arg Glu Ser Leu Ser Xaa Arg Ser Trp His
                      -25   -20

TTG CCA GCT TCT TTG ATG ATG GCC CAG GKA TTT ATA CCA GCT GTA GCA   341
Leu Pro Ala Ser Leu Met Met Ala Gln Xaa Phe Ile Pro Ala Val Ala
  -15   -10   -5

AAA GTA GGA   350
Lys Val Gly
  1

(2) INFORMATION FOR SEQ ID NO: 224:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 430 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 226..295
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 95
                                region 121..190
                                id W07343
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 251..424
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 5.4
                                seq LSLHLLATRACYG/IL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:
```

```
AACAGGTGGT TGCAGAAGTT TCGTGGTGTC GGGCGCGCGT CTGCACTGCA GACGCAGAGG    60

GTTTGGGAGC GAGCAGTTTC CTGCCCAGGG ATGGGGGTCC TGGCTGCACT TCACGGGGGC   120

GGCCCTTTCG TTTCGCTCTG CGTGACAGGT CTCGCTTGAT TGGGTTTCTC ATGGGTSKCT   180

GGCGTTTCTA CGGCGCGGCT CTCACGGACT CAGGCCAGGC CACTCGCAGG ATTAATTGGA   240

ATTCTTCAAA ATG TCA GGT GTG GTA CCC ACA GCC CCT GAA CAG CCT GCA     289
            Met Ser Gly Val Val Pro Thr Ala Pro Glu Gln Pro Ala
                -55                      -50

NGT GAA ATG GAA AAT CAA ACA AAA CCA CCA GAT CCA AGG CCT GAT GCT    337
Xaa Glu Met Glu Asn Gln Thr Lys Pro Pro Asp Pro Arg Pro Asp Ala
-45               -40              -35                  -30

CCT CCT GAA TAC AGT TCT CAT DBG TTT ACC AGG ACC CCC TGG AAA CAG    385
Pro Pro Glu Tyr Ser Ser His Xaa Phe Thr Arg Thr Pro Trp Lys Gln
            -25              -20                  -15

CTG TCC CTC CAC CTA CTG GCT ACC AGA GCT TGC TAT GGG ATA CTA        430
Leu Ser Leu His Leu Leu Ala Thr Arg Ala Cys Tyr Gly Ile Leu
            -10              -5                    1
```

```
(2) INFORMATION FOR SEQ ID NO: 225:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 387 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(75..325)
```

```
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 100
                                         region 82..332
                                         id AA004751
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: complement(88..255)
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 97
                                         region 153..320
                                         id N27443
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: complement(18..105)
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 94
                                         region 304..391
                                         id N27443
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: complement(258..325)
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 100
                                         region 81..148
                                         id N27443
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: complement(22..325)
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 99
                                         region 80..383
                                         id AA015608
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: complement(78..253)
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 99
                                         region 165..340
                                         id H09727
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: complement(253..285)
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:   identity 96
                                         region 132..164
                                         id H09727
                                         est

        (ix) FEATURE:
```

```
              (A) NAME/KEY: other
              (B) LOCATION: complement(49..276)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:  identity 97
                                      region 133..360
                                      id AA027099
                                      est

         (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: complement(269..325)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:  identity 100
                                      region 83..139
                                      id AA027099
                                      est

         (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 139..369
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 5.3
                                      seq TWVFTCLVFFCFG/LS


         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:


AGAAACAGGG AGAAGAGGAA GGCTAGAAGC CTGAGCAAGT GAGGGTAGAA CCTTTTGGGA    60

CTGGCCTTTG AAGCTCTGGC CAGGGATGGG GTGGGGGCCA AAAGGACAGA GCCTGGTATG   120

TCTTCATAGT CATTGAGA ATG TGG AGA TAC CAG TTT GGG TGG GGG GTG ATC   171
                    Met Trp Arg Tyr Gln Phe Gly Trp Gly Val Ile
                    -75                     -70

ACC AGG GGA CCT AGG GAG ATC CCC TTC CCA CCC TCT CTG TTG GCC TCA   219
Thr Arg Gly Pro Arg Glu Ile Pro Phe Pro Pro Ser Leu Leu Ala Ser
-65                 -60                     -55

GAG TCA CTC CTG CCC CCT CTC CCT GAC TTG GTG CTC ACA TGC ACC TCA   267
Glu Ser Leu Leu Pro Pro Leu Pro Asp Leu Val Leu Thr Cys Thr Ser
-50                 -45                     -40                 -35

CTA GGG TTT GTG ACC AGG GTC TGG ATG AGC TTG AAT TTG AAT GAA TTG   315
Leu Gly Phe Val Thr Arg Val Trp Met Ser Leu Asn Leu Asn Glu Leu
            -30                 -25                     -20

AGT TTG TAT TCT AGA ACC TGG GTT TTT ACA TGT TTG GTC TTT TTT TGT   363
Ser Leu Tyr Ser Arg Thr Trp Val Phe Thr Cys Leu Val Phe Phe Cys
        -15                 -10                     -5

TTT GGK TTG TCA MCC TCG CTA GGG                                    387
Phe Gly Leu Ser Xaa Ser Leu Gly
        1               5



    (2) INFORMATION FOR SEQ ID NO: 226:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 300 base pairs
```

```
      . (B)  TYPE: NUCLEIC ACID
       (C)  STRANDEDNESS: DOUBLE
       (D)  TOPOLOGY: LINEAR

  (ii)  MOLECULE TYPE: CDNA

  (vi)  ORIGINAL SOURCE:
        (A)  ORGANISM: Homo Sapiens
        (F)  TISSUE TYPE: Brain

  (ix)  FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 123..295
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 97
                                 region 121..293
                                 id N78275
                                 est

  (ix)  FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 43..128
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 100
                                 region 40..125
                                 id N78275
                                 est

  (ix)  FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 19..295
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 99
                                 region 4..280
                                 id R35388
                                 est

  (ix)  FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 40..295
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 98
                                 region 14..269
                                 id W03418
                                 est

  (ix)  FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 29..283
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 98
                                 region 27..281
                                 id HSC29H041
                                 est

  (ix)  FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 49..266
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 96
                                 region 78..295
```

id R60376
est

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 184..270
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION: score 5.2
                              seq FFMLLGSLLPVKI/IE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

AAGACTGCGC GGCCGTWGGG CGTGCAGCGG CGCCAGTCGG CGGACGAGGG GCCCCCGGGA   60

GTTGCTGGAC TGAGACATGA GCCTCCAACT GTGTGGTTGG GCTCGGTAGC ACATCGTGGG   120

ACTTGGGTGT GCGCCCACAG ATGGTTTGGC CCTGCAGTGA CCAGAGCAGC CCAAGCCGCC   180

ACC ATG GTG AAA TTG CTA GTG GCC AAA ATC CTG TGC ATG GTG GGC GTG   228
    Met Val Lys Leu Leu Val Ala Lys Ile Leu Cys Met Val Gly Val
            -25   -20   -15

TTC TTC TTC ATG CTG CTC GGC TCC CTG CTC CCC GTG AAG ATC ATC GAG   276
Phe Phe Phe Met Leu Leu Gly Ser Leu Leu Pro Val Lys Ile Ile Glu
        -10   -5   1

ACA GAT TTT GAG AAG GCC CCA GGG   300
Thr Asp Phe Glu Lys Ala Pro Gly
        5   10

(2) INFORMATION FOR SEQ ID NO: 227:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 76 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(2..73)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 40..111
                                  id HSC39G092
                                  est

      (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(2..73)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98

region 37..108
id T89094
est

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 11..61
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 5.2
                                     seq IMCLIGLKANASS/ET

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ATCCTTTTGC ATG CCT GTT TCT ATC ATG TGC TTG ATA GGC CTC AAA GCT   49
           Met Pro Val Ser Ile Met Cys Leu Ile Gly Leu Lys Ala
                -15   -10   -5

AAT GCT TCC AGT GAA ACA CAC TCA GGG   76
Asn Ala Ser Ser Glu Thr His Ser Gly
              1   5

(2) INFORMATION FOR SEQ ID NO: 228:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 125 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 11..120
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 100
                                     region 1..110
                                     id HSC3IG111
                                     est

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 48..98
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 5.2
                                     seq LLYLVLEKLVSRA/FQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

AGATACTAAT CCTTTAAAAA AGTGTAAATG GAGAAAAGTT ATATTTT ATG AAG GTT   56
                                                     Met Lys Val
                                                     -15

```
ATT TTG TTG TAT TTA GTA TTG GAA AAG TTG GTT TCC AGA GCA TTT CAG        104
Ile Leu Leu Tyr Leu Val Leu Glu Lys Leu Val Ser Arg Ala Phe Gln
            -10                 -5                  1

AAT GTC GAA GCA CCA CAC GGG                                           125
Asn Val Glu Ala Pro His Gly
        5
```

(2) INFORMATION FOR SEQ ID NO: 229:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 170 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 81..170
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 97
                                    region 54..143
                                    id T09307
                                    est

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 29..81
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 92
                                    region 1..53
                                    id T09307
                                    est

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 12..77
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 98
                                    region 1..66
                                    id AA159859
                                    est

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 28..75
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                    region 1..48
                                    id H13321
                                    est

       (ix) FEATURE:

```
     (A) NAME/KEY: other
     (B) LOCATION: 15..75
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 93
                             region 10..70
                             id W02365
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 33..77
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 95
                             region 1..45
                             id AA113927
                             est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 33..89
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 5.1
                             seq LLLGGRVCXPSLA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:
```

```
AAGCCGAYYG CTGAAGGCTG GTTTGCGTCG AC ATG GCG GTT ACC CTG AGT CTC        53
                                     Met Ala Val Thr Leu Ser Leu
                                                         -15

TTG CTG GGC GGG CGC GTT TGC SCG CCG TCA CTC GCT GTG GGT TCG CGA       101
Leu Leu Gly Gly Arg Val Cys Xaa Pro Ser Leu Ala Val Gly Ser Arg
         -10                 -5                      1

CCC GGG GGG TGG CGG GCC CAG GCC CTA TTG GCC GGG AGC CGG ACC CCG       149
Pro Gly Gly Trp Arg Ala Gln Ala Leu Leu Ala Gly Ser Arg Thr Pro
  5               10                  15                    20

ATT CCG ACT GGG AAC CGG AGG                                           170
Ile Pro Thr Gly Asn Arg Arg
                25
```

```
(2) INFORMATION FOR SEQ ID NO: 230:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 263 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: other
```

```
            (B) LOCATION: 57..261
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 97
                                    region 40..244
                                    id R59037
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(184..237)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 100
                                    region 38..91
                                    id R67654
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 117..185
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.1
                                    seq LLPELGVVTPAQG/PR

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:


AAGACCATCA ACTATGGAAA GGAGATCTAG GGAACACCGT CTTGAACCCG CCAGGGTTTT    60

GAGTCTCGGA CCCAGGAGAT CCAACCCTGA CCACCCTCCC AGGATGCAGC AGGGGG ATG   119
                                                              Met

TTA AAT CAG ACT TCA GGA AGA ACT TCC TTG CTG CCT GAG TTA GGT GTC   167
Leu Asn Gln Thr Ser Gly Arg Thr Ser Leu Leu Pro Glu Leu Gly Val
     -20             -15             -10

GTC ACG CCT GCC CAG GGG CCA AGG AGG CGG GTT TGG TGC GGC CAC TCC   215
Val Thr Pro Ala Gln Gly Pro Arg Arg Arg Val Trp Cys Gly His Ser
     -5               1               5               10

AAG GCC AAA GCG AGA AAA TCT TAC TGC GCA CGC GCA ATA GAC TGC CAG   263
Lys Ala Lys Ala Arg Lys Ser Tyr Cys Ala Arg Ala Ile Asp Cys Gln
           15               20               25



(2) INFORMATION FOR SEQ ID NO: 231:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 430 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

      (ix) FEATURE:
            (A) NAME/KEY: other
```

```
(B) LOCATION: 99..416
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
                       region 1..318
                       id T31969
                       est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 49..334
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 99
                            region 2..287
                            id HSB03B072
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(2..57)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 100
                            region 1..56
                            id W51830
                            est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 26..262
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 5
                            seq SFLGFSAPTPIQA/LT
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```
ATGTGATGAT CCGGAGGCTG GGGAG ATG ACA TCA GAA AAC CTG GTC CAA ACT     52
                             Met Thr Ser Glu Asn Leu Val Gln Thr
                                             -75

GCT CCA AAA AAG AAG AAA AAT AAA GGG AAA AAA GGG TTG GAG CCT TCT    100
Ala Pro Lys Lys Lys Lys Asn Lys Gly Lys Lys Gly Leu Glu Pro Ser
-70                 -65             -60                 -55

CAG AGC ACT GCT GCC AAG GTG CCC AAA AAA GCG AAG ACA TGG ATT CCT    148
Gln Ser Thr Ala Ala Lys Val Pro Lys Lys Ala Lys Thr Trp Ile Pro
                -50             -45             -40

GAA GTT CAT GAT CAG AAA GCA GAT GTG TCA GCT TGG AAG GAC CTG TTT    196
Glu Val His Asp Gln Lys Ala Asp Val Ser Ala Trp Lys Asp Leu Phe
            -35             -30             -25

GTT CCC AGG CCG GTT CTC CGA GCA CTC AGC TTT CTA GGC TTC TCT GCA    244
Val Pro Arg Pro Val Leu Arg Ala Leu Ser Phe Leu Gly Phe Ser Ala
        -20             -15             -10

CCC ACA CCA ATC CAA GCC CTG ACC TTG GCA CCT GCC ATC CGT GAC AAA    292
Pro Thr Pro Ile Gln Ala Leu Thr Leu Ala Pro Ala Ile Arg Asp Lys
    -5              1               5                   10

CTG GAC ATC CTT GGG GCT GCT GAG ACA GGA AGT GGG AAA ACT CTT GCC    340
Leu Asp Ile Leu Gly Ala Ala Glu Thr Gly Ser Gly Lys Thr Leu Ala
```

```
                15·              20              25

TTT GCC ATC CCA ATG ATT CAT GCG GTG TTG CAG TGG CAG AAG AGG AAT    388
Phe Ala Ile Pro Met Ile His Ala Val Leu Gln Trp Gln Lys Arg Asn
            30              35              40

GCT GCC CCT CCT CCA AGT AAC ACC GAA GCA CCA CCT GGA GAG            430
Ala Ala Pro Pro Pro Ser Asn Thr Glu Ala Pro Pro Gly Glu
        45              50              55
```

(2) INFORMATION FOR SEQ ID NO: 232:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 1..37
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                           region 9..45
                           id W84513
                           est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 16..84
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.9
                           seq WHXLIPLTWACMA/RQ

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
AATCTTCTCC GCGCT ATG GCT GCG TTC GGC CGT CAG SCW TTS ART TGG CAC    51
                  Met Ala Ala Phe Gly Arg Gln Xaa Xaa Xaa Trp His
                      -20                     -15

CKY CTG ATC CCC CTC ACC TGG GCC TGT ATG GCT AGG CAG ACT CCT CAT    99
Xaa Leu Ile Pro Leu Thr Trp Ala Cys Met Ala Arg Gln Thr Pro His
    -10              -5               1               5

CTT GGA GAA CAG AGA AGG ACG ACA GCT TCT TTG TKG CGC AAA CTG ACT    147
Leu Gly Glu Gln Arg Arg Thr Thr Ala Ser Leu Xaa Arg Lys Leu Thr
                10              15              20

ACA GCC TCC AAT GGA GGG GTC ATT GAG GAG TTA TCT TGT GTK AGA TCC    195
Thr Ala Ser Asn Gly Gly Val Ile Glu Glu Leu Ser Cys Val Arg Ser
            25              30              35
```

AAT AAC TAT GTG CAG GAA CCA GAG TGC AGG AGG AAT CTT GTT CAG TGC   243
Asn Asn Tyr Val Gln Glu Pro Glu Cys Arg Arg Asn Leu Val Gln Cys
        40   45   50

CTC CTC TGG   252
Leu Leu Trp
    55

(2) INFORMATION FOR SEQ ID NO: 233:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 347 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 44..187
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 96
                                        region 1..144
                                        id AA151232
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 187..285
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 97
                                        region 143..241
                                        id AA151232
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 314..349
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 100
                                        region 272..307
                                        id AA151232
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 39..225
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 95
                                        region 2..188
                                        id AA040887
                                        est

        (ix) FEATURE:

        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 144..314
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.9
                                seq GWFLSGCPHGSSA/TW

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

AATGGGGATG TTGAATTTGG AAATTGGAGG GGACGCTGGT GGWYKKATTG GGTGCAAGGA   60

GTTGGTGTTG ATGGAGGAGC AGGASRCCAG AGTCCCAGCC CTGGAACCGT TCAGAGTGGA   120

GCAGGCACCA CCTGTAATCT ACT ATG TCC CTG ACT TCA TCT CCA AAG AAG AGG   173
                         Met Ser Leu Thr Ser Ser Pro Lys Lys Arg
                             -55   -50

AGG AGT ATT TGC TTC GAC AGG TTT TTA ATG CCC CAA AGC CAA AGT GGA   221
Arg Ser Ile Cys Phe Asp Arg Phe Leu Met Pro Gln Ser Gln Ser Gly
        -45   -40   -35

CCC AGC TCT CTG GGA GAA AGT TAC AGA ACT GGG GTG GGC TTC CTC ATC   269
Pro Ser Ser Leu Gly Glu Ser Tyr Arg Thr Gly Val Gly Phe Leu Ile
    -30   -25   -20

CCC GAG GGA TGG TTC CTG AGC GGC TGC CCC CAT GGC TCC AGC GCT ACG   317
Pro Glu Gly Trp Phe Leu Ser Gly Cys Pro His Gly Ser Ser Ala Thr
-15   -10   -5   1

TGG ACA AAG TGT CAA ACC TCA GCC TCT TTG   347
Trp Thr Lys Cys Gln Thr Ser Ala Ser Leu
        5   10

(2) INFORMATION FOR SEQ ID NO: 234:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 227 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 115..226
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 95
                                    region 135..246
                                    id HSC0GF021
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 90..206

```
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.8
                                seq SLXFCLSPPPSPS/LR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:


AAACCCCATA CCCCCTCCCC ATCTTGTGAT CACCCTCATT ACCTCTTCTG GGCCCCCTGT    60

GGACCTGCGT TGACCCAGCA TGGGCTACA ATG GGG GAG TTG GGT AAT CGC TCC    113
                                Met Gly Glu Leu Gly Asn Arg Ser
                                                    -35

CGT TGC ATC CTG TTT CTG TCT GAA AAC CCT TGT CTT TCT GAA TCC ATC    161
Arg Cys Ile Leu Phe Leu Ser Glu Asn Pro Cys Leu Ser Glu Ser Ile
    -30             -25                 -20

TTT CAG TCT CTS RCA TTC TGT CTT TCC CCT CCT CCT TCA CCT TCC CTC    209
Phe Gln Ser Leu Xaa Phe Cys Leu Ser Pro Pro Pro Ser Pro Ser Leu
-15             -10                 -5                          1

CGT CCC TCT CCC TCA CGG                                            227
Arg Pro Ser Pro Ser Arg
            5



(2) INFORMATION FOR SEQ ID NO: 235:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 430 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 101..355
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 83..337
                                id AA057242
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 57..101
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 40..84
                                id AA057242
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
```

```
                (B) LOCATION: 357..400
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 100
                                        region 338..381
                                        id AA057242
                                        est

         (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 18..51
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 100
                                        region 1..34
                                        id AA057242
                                        est

         (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 400..431
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 100
                                        region 382..413
                                        id AA057242
                                        est

         (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 84..218
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 97
                                        region 73..207
                                        id R09808
                                        est

         (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 10..51
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 100
                                        region 1..42
                                        id R09808
                                        est

         (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 98..376
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION:  score 4.7
                                        seq VLLLRQXFAQAEK/WY

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:


AATTTTCYGT GGTCCAACTA CCCTCGGCGA TCCCAGGCTT GGCGGGGCAC CGCCTGGCCT   60

CTCCCGTTCC TTTAGGCTGC CGCCGCTGCC TGCCGCC ATG GCA GAG TTG GGC CTA   115
                                        Met Ala Glu Leu Gly Leu
                                                        -90

AAT GAG CAC CAT CAA AAT GAA GTT ATT AAT TAT ATG CGT TTT GCT CGT   163
Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg
```

```
                 -85                    -80                     -75

TCA AAG AGA GGC TTG AGA CTC AAA ACT GTA GAT TCC TGC TTC CAA GAC    211
Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp
    -70                    -65                     -60

CTC AAG GAG AGC AGG CTG GTG GAG GAC ACC TTC ACC ATA GAT GAA GTC    259
Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val
-55                    -50                     -45                     -40

TCT GAA GTC CTC AAT GGA TTA CAA GCT GTG GTT CAT AGT GAG GTG GAA    307
Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu
                   -35                    -30                     -25

TCT GAG CTC ATC AAC ACT GCC TAT ACC AAT GTG TTA CTT CTG CGA CAG    355
Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Leu Arg Gln
              -20                    -15                     -10

NTG TTT GCA CAA GCT GAG AAG TGG TAT CTT AAG CTA CAG ACA GAC ATC    403
Xaa Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile
         -5                     1                      5

TCT GAA CTT GAA AAC CGA GAA TTA TTA                                430
Ser Glu Leu Glu Asn Arg Glu Leu Leu
10                    15
```

(2) INFORMATION FOR SEQ ID NO: 236:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 344 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 20..231
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                           region 1..212
                           id N33729
                           est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 135..281
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.6
                           seq SWAVGLLYAVAQG/SK

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
AATTAGCGAG GCCATGGGGG AAAAAGTCTA ACTGGCGGAA CTCCTGGGAA CTGGGGCGAT    60

GGGCTCTTAG TATCGGAGGA TTGGAGCCAT CTGATTTTTA CCTGAAATTC CTTAGTCTCT   120

CCTGTGTTGG GGAA ATG GTC ACC TTG CCT TCA GGG ACC TGG GCT TTC AGC    170
              Met Val Thr Leu Pro Ser Gly Thr Trp Ala Phe Ser
                          -45                 -40

TGT CCA TAC CTG GCC CTG GTT GAT GGC GGC ATG CTG GGC AGT GCA CGT   218
Cys Pro Tyr Leu Ala Leu Val Asp Gly Gly Met Leu Gly Ser Ala Arg
        -35             -30             -25

GAA GAC GCA CAT GCA TCT GTT GTT TCC TGG GCA GTT GGT CTT CTT TAT   266
Glu Asp Ala His Ala Ser Val Val Ser Trp Ala Val Gly Leu Leu Tyr
    -20             -15             -10

GCA GTG GCT CAG GGC TCC AAG AGA AGG AAA GTG CAA GAT GTC AAG CCT   314
Ala Val Ala Gln Gly Ser Lys Arg Arg Lys Val Gln Asp Val Lys Pro
-5              1               5               10

CTT NGT TGG TCA AGA ACT GGC ACC CTC GGG                           344
Leu Xaa Trp Ser Arg Thr Gly Thr Leu Gly
        15              20
```

(2) INFORMATION FOR SEQ ID NO: 237:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 419 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 116..419
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 98
                                     region 122..425
                                     id W68799
                                     est

       (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 18..117
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 97
                                     region 1..100
                                     id W68799
                                     est

       (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 18..209

```
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 93
                                 region 1..192
                                 id W49697
                                 est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 199..290
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 95
                             region 183..274
                             id W49697
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 291..367
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 276..352
                             id W49697
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 387..417
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 374..404
                             id W49697
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 48..419
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                             region 1..372
                             id AA149518
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 171..414
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 116..359
                             id W17032
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 57..174
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 1..118
                             id W17032
                             est

(ix) FEATURE:
```

                (A) NAME/KEY: other
                (B) LOCATION: 78..386
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 98
                                        region 1..309
                                        id W78749
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 386..419
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 100
                                        region 310..343
                                        id W78749
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 180..383
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 4.6
                                        seq LPFSLVSMLVTQG/LV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

AAGACAGGTG GGGTACTCGG GAAGCTGGAG CGGGCCGGCG GTGCAGTCAC GGGGGAGCGA   60

GGCCTGCTGG GCTTGGCAAC GAGGGACTCG GCCTCGGAGG CGACCCAGAC CACACAGACA   120

CTGGGTCAAG GAGTAAGCAG AGGATAAACA ACTGGAAGGA GAGCAAGCAC AAAGTCATC   179

ATG GCT TCA GCG TCT GCT CGT GGA AAC CAA GAT AAA GAT GCC CAT TTT   227
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
            -65   -60   -55

CCA CCA CCA AGC AAG CAG AGC CTG TTG TTT TGT CCA AAA TMH NNA CTG   275
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Xaa Xaa Leu
            -50   -45   -40

CAC ATC CAC AGA GCA GAG ATC TCA AAG ATT ATG CGA GAA TGT CAG GAA   323
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
    -35   -30   -25

GAA AGT TTC TGG AAG AGA GCT CTG CCT TTT TCT CTT GTA AGC ATG CTT   371
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20   -15   -10   -5

GTC ACC CAG GGA CTA GTC TAC CAA GGT TAT TTG GCA GCT AAT TCT AGA   419
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
                1   5   10

(2) INFORMATION FOR SEQ ID NO: 238:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 274 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE

.(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(37..269)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 99
                         region 2..234
                         id AA147071
                         est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(2..31)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 93
                         region 239..268
                         id AA147071
                         est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(37..269)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 99
                         region 58..290
                         id H98153
                         est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(2..31)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 93
                         region 295..324
                         id H98153
                         est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(37..269)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 98
                         region 59..291
                         id N49401
                         est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(2..31)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 93
                         region 296..325
                         id N49401
                         est

```
     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(87..269)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 99
                                  region 37..219
                                  id N80022
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 62..268
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 4.5
                                  seq FILSLCVLCIVLT/TG

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:
```

```
AATTAAGTCA KDATACAAAT CAGCACAGAT AACGDMAATG TTTCCAATAT WWTAAAATGT    60

A ATG TTA CTT ATG AAA AGT ATT TTG CTT AAG GTT GTG TGT GTA TTG TGT   109
  Met Leu Leu Met Lys Ser Ile Leu Leu Lys Val Val Cys Val Leu Cys
              -65               -60                 -55

ATA TAC CTC AAG TTC AAG TTA ATG GCA TTG ATT TAT GTT CCA GAC AAA     157
Ile Tyr Leu Lys Phe Lys Leu Met Ala Leu Ile Tyr Val Pro Asp Lys
          -50               -45                 -40

AAT AAC ACA AAT AAT AAT ATC CTT CGT TAT AAC CAC AAT GAG ATA AGT     205
Asn Asn Thr Asn Asn Asn Ile Leu Arg Tyr Asn His Asn Glu Ile Ser
          -35               -30                 -25

ATT GGC ATT AGT GTT CAG TGC CAT TTT ATA CTT TCT CTC TGT GTT CTC     253
Ile Gly Ile Ser Val Gln Cys His Phe Ile Leu Ser Leu Cys Val Leu
     -20               -15                 -10

TGT ATT GTA CTA ACC ACT GGG                                          274
Cys Ile Val Leu Thr Thr Gly
-5                    1
```

```
(2) INFORMATION FOR SEQ ID NO: 239:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 249 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: CDNA

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 100..249
```

```
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 94
                                        region 20..169
                                        id N41898
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 113..249
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION:  identity 94
                                        region 38..174
                                        id H69272
                                        est

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 100..147
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION:  score 4.5
                                        seq RLLLRRFLASVIS/RK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:


AGTTATGTAC GTTCCCCCCC CCGAGGAAGT GAYGACAGGC GTGCCCTTGA CAGGCAGGGA    60

GGGCTAGGCT GTGCATCCCT CCGCTCGCAT TGCAGGGAG ATG GCT CAG CGA CTT       114
                                            Met Ala Gln Arg Leu
                                                           -15

CTT CTG AGG AGG TTC CTG GCC TCT GTC ATC TCC AGG AAG CCC TCT CAG     162
Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser Arg Lys Pro Ser Gln
   -10               -5                  1                   5

GGT CAG TGG CCA CCC CTC ACT TCC AGA GCC CTG CAG ACC CCA YAA TGC     210
Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu Gln Thr Pro Xaa Cys
               10                  15                  20

AGT YCT GGT GGC CTG ACT GTA ACA CCC AAC CCA AGC CGG              249
Ser Xaa Gly Gly Leu Thr Val Thr Pro Asn Pro Ser Arg
        25                  30
```

(2) INFORMATION FOR SEQ ID NO: 240:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 310 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: other

```
     (B) LOCATION: 51..209
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 99
                              region 49..207
                              id N56053
                              est


(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 2..54
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 96
                              region 1..53
                              id N56053
                              est


(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 211..246
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 100
                              region 208..243
                              id N56053
                              est


(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 275..307
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 96
                              region 270..302
                              id N56053
                              est


(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 51..178
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 98
                              region 44..171
                              id R59444
                              est


(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 212..275
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 100
                              region 203..266
                              id R59444
                              est


(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 7..54
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 95
                              region 1..48
                              id R59444
                              est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 274..308
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 100
                              region 266..300
                              id R59444
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 178..209
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 100
                              region 170..201
                              id R59444
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 51..178
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 98
                              region 45..172
                              id AA156837
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 178..246
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 100
                              region 171..239
                              id AA156837
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 247..308
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 100
                              region 239..300
                              id AA156837
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 6..54
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 95
                              region 1..49
                              id AA156837
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 51..178
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 99
                              region 56..183
                              id N88392
```

                                            est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 13..54
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 95
                                  region 19..60
                                  id N88392
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 247..285
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 249..287
                                  id N88392
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 211..246
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 214..249
                                  id N88392
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 179..209
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 183..213
                                  id N88392
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 7..209
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 1..203
                                  id R18752
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 211..246
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 204..239
                                  id R18752
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 2..232
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:. score 4.4

seq FEARIALLPLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

A ATG GCG GCG TCA AAG GTG AAG CAG GAC ATG CCT CCR MCG GGG GGC TAT   49
  Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Xaa Gly Gly Tyr
      -75   -70   -65

GGG CCC ATC GAC TAC AAA CGG AAC TTG CCG CGT CGA GGA CTG TCG GGC   97
Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
    -60   -55   -50

TAC AGC ATG CTG GCC ATA GGG ATT GGA ACC CTG ATC TAC GGG CAC TGG   145
Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
-45   -40   -35   -30

AGC ATA ATG AAG TGG AAC CGT GAG CGC AGG CGC CTA CAA ATC GAG GAC   193
Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
            -25   -20   -15

TTC GAG GCT CGC ATC GCG CTG TTG CCA CTG TTA CAG GCA GAA ACC GAC   241
Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
        -10   -5   1

CGG AGG ACC TTG CAG ATG CTT CGG GAG AAC CTG GAG GAG GAG GCC ATC   289
Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
    5   10   15

ATC ATG AAG GAC GTG CCC GGA   310
Ile Met Lys Asp Val Pro Gly
20   25

(2) INFORMATION FOR SEQ ID NO: 241:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 388 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 93..257
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                    region 103..267
                                    id H87397
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 158..319

       (C) IDENTIFICATION METHOD: Von Heijne matrix
       (D) OTHER INFORMATION: score 4.3
                             seq LLSLAILSHISTP/GC

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:


```
AGACAAAGAG AAGGCAAAAT SAGTTTGTGT CCCTGAGTTG CTAAGTGGAG AAGAAACGTC   60

CACCAACCAG GAAACACCTG CCTCCAACTG TTAATAGGTC TGTGAAATGT GCTTTGTTTC   120

TGGTCAGCAT GGACACCCGC TTTAATAGTG GCTTCAG ATG AGG CAC CTT GTG ACA   175
                                       Met Arg His Leu Val Thr
                                                        -50

GAG GAG CTC TTC CCC TGC AGC AAC CTT GAA GAT GTT GTG GAA GAC AAT   223
Glu Glu Leu Phe Pro Cys Ser Asn Leu Glu Asp Val Val Glu Asp Asn
         -45             -40              -35

AGC CAT TCT TAC TTC ACT CTG AGG ATC ACG ATG GCG TGC AAG GGT GTG   271
Ser His Ser Tyr Phe Thr Leu Arg Ile Thr Met Ala Cys Lys Gly Val
         -30             -25              -20

CCA AGC ACA TTG CTA TCT TTG GCC ATT CTC TCT CAC ATT AGT ACA CCT   319
Pro Ser Thr Leu Leu Ser Leu Ala Ile Leu Ser His Ile Ser Thr Pro
         -15             -10               -5

GGA TGT GAA TGG CAC GTT ATC TAT GTA AGC AGT BAT GGT CTC TAT CTT   367
Gly Cys Glu Trp His Val Ile Tyr Val Ser Ser Xaa Gly Leu Tyr Leu
  1          5                 10               15

GTG GTA GAA ATG ACA GAC CGG                                       388
Val Val Glu Met Thr Asp Arg
         20
```


(2) INFORMATION FOR SEQ ID NO: 242:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 391 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 108..392
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                             region 104..388
                             id T08101
                             est

      (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 32..110
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                               region 1..79
                               id T08101
                               est

 (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 108..392
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                               region 39..323
                               id T27149
                               est

 (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 113..392
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                               region 30..309
                               id H06555
                               est

 (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 108..316
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                               region 90..298
                               id HSC3CC081
                               est

 (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 60..110
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 94
                               region 15..65
                               id HSC3CC081
                               est

 (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 105..316
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 99
                               region 58..269
                               id T74159
                               est

 (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 76..105
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 93
                               region 5..34
                               id T74159
                               est
```

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 152..379
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 4.3
                                    seq FRLLXVFAYGTYA/DY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AAGTGGCCAG AGCGACTCTT CAGGGAGGTG GCAGGAAAGG CTTGGAACAG CTGCCGGAGG   60

TGACGGAGCG GCGGCCCCGC CCGGTGCGCT GGAGGTCGAA GCTTCCAGCT CTGGACATCC   120

TGAGCCCAAG TCCCCCACAC TCAGTGCAGT G ATG AGT GCG GAA GTG AAG GTG   172
                                   Met Ser Ala Glu Val Lys Val
                                   -75   -70

ACA GGG CAG AAC CAG GAG CAA TTT CTG CTC CTA GCC AAG TCG GCC AAG   220
Thr Gly Gln Asn Gln Glu Gln Phe Leu Leu Leu Ala Lys Ser Ala Lys
        -65   -60   -55

GGG GCA GCG CTG GCC ACA CTC ATC CAT CAG GTG CTG GAG GCC CCT GGT   268
Gly Ala Ala Leu Ala Thr Leu Ile His Gln Val Leu Glu Ala Pro Gly
        -50   -45   -40

GTC TAC GTG TTT GGA GAA CTG CTG GAC ATG CCC AAT GTT AGA GAG CTG   316
Val Tyr Val Phe Gly Glu Leu Leu Asp Met Pro Asn Val Arg Glu Leu
        -35   -30   -25

GCT GAG AGT NAC TTT GCC TCT ACC TTC CGG CTG CTC AMA GTG TTT GCT   364
Ala Glu Ser Xaa Phe Ala Ser Thr Phe Arg Leu Leu Xaa Val Phe Ala
        -20   -15   -10

TAT GGG ACA TAC GCT GAC TAC TWA GCT   391
Tyr Gly Thr Tyr Ala Asp Tyr Xaa Ala
-5   1

(2) INFORMATION FOR SEQ ID NO: 243:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 299 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 47..248
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 97
                                    region 15..216

```
                              id HUM429E03B
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 244..299
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 94
                             region 211..266
                             id HUM429E03B
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 133..299
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 107..273
                             id T80259
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 47..139
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 92
                             region 22..114
                             id T80259
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 48..292
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 94
                             region 1..245
                             id T31768
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 111..299
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 94
                             region 47..235
                             id N32697
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 64..106
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 1..43
                             id N32697
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 74..299
     (C) IDENTIFICATION METHOD: blastn
```

```
            (D) OTHER INFORMATION:  identity 94
                                    region 1..226
                                    id N44613
                                    est

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 165..266
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 4.3
                                 seq QLFAFLNLLPVEA/DI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:
```

ACTTCCGCTT CGCCTAGGTG TTGTCGTCCC TGCTAGTACT CCGGGCTGGG GGTCGGTGCG   60

GATATTCAGT CATGAAATCA SGGTAGGGAC TTCTCCCGCA GCGACGCGGC TGGCAAGACT   120

GTTTGTGTWG CGGGGGCCGG ACTTCAAGGT GATTTTACAA CGAG ATG CTG CTC TCC   176
                                                   Met Leu Leu Ser

ATA GGG ATG CTC ATG CTG TCA GCC ACA CAA GTS TAS ACC ATC TTG AST   224
Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Xaa Thr Ile Leu Xaa
-30   -25   -20   -15

GTC CAG CTC TTT GCA TTC TTA AAC CTA CTG CCT GTA GAA GCA GAC ATT   272
Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val Glu Ala Asp Ile
             -10   -5   1

KTA GCA TAT AAC TTT GAA AAT GCA TCT   299
Xaa Ala Tyr Asn Phe Glu Asn Ala Ser
         5   10


```
(2) INFORMATION FOR SEQ ID NO: 244:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 312 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(115..313)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 98
                                     region 1..199
                                     id H19659
                                     est

        (ix) FEATURE:
             (A) NAME/KEY: other
```

```
            (B) LOCATION: complement(2..102)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 97
                                    region 212..312
                                    id H19659
                                    est


    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(115..313)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 97
                                    region 1..199
                                    id R72881
                                    est


    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(115..290)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 1..176
                                    id H50517
                                    est


    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(44..102)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 100
                                    region 189..247
                                    id H50517
                                    est


    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(115..302)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 96
                                    region 36..223
                                    id H41556
                                    est


    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(115..313)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 95
                                    region 2..200
                                    id R71794
                                    est


    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(44..102)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 96
                                    region 213..271
                                    id R71794
                                    est
```

```
        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 229..276
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 4.2
                                      seq EVVSLSYCGVSWG/RI

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:


ACATTTCTGC TCAGATTCCC GCCATCTCCA TTGCATTCAT GTACTACCCT CAGTCTACAC   60

TCACAATCAT CTTCTCCCAA GACTGCTCCC TTTTGTTTTG TGTTTTTTTG AGGGGAATTA  120

AGGAAAAATA AGTGGGGGCA GGTTTGGAGA GCTGCTTCCA GTGGATAGTT GATGAGAATC  180

CTGACCAAAG GAAGGCACCC TTGACTGTYG GGATAGACAG ATGGACCT ATG GGG TGG   237
                                                      Met Gly Trp
                                                       -15

GAG GTG GTG TCC CTT TCA TAC TGT GGT GTC TCT TGG GGA AGG ATC TCC   285
Glu Val Val Ser Leu Ser Tyr Cys Gly Val Ser Trp Gly Arg Ile Ser
           -10                 -5                      1

CCG AAT CTC AAT AAA CCA GTG AAC AGG                                312
Pro Asn Leu Asn Lys Pro Val Asn Arg
 5                 10


(2) INFORMATION FOR SEQ ID NO: 245:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 252 base pairs
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: DOUBLE
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 41..210
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION:  identity 98
                                      region 77..246
                                      id R59124
                                      est

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 37..132
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 4.2
                                      seq CWELFCLEHGIQA/DG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:
```

```
AAAGCTGAGA GGKGCGCGGG CGAGGACAGC GGCASR ATG CGG GAA TGC ATA TCA        54
                                          Met Arg Glu Cys Ile Ser
                                              -30

GTC CAC GTG GGC CAA GCG GGA GTD CAG ATT GGC AAT GCC TGC TGG GAG       102
Val His Val Gly Gln Ala Gly Val Gln Ile Gly Asn Ala Cys Trp Glu
    -25                 -20                 -15

CTC TTC TGC CTG GAA CAC GGC ATC CAG GCA GAC GGC ACT TTT GAT GCT      150
Leu Phe Cys Leu Glu His Gly Ile Gln Ala Asp Gly Thr Phe Asp Ala
-10                 -5                   1                 5

CAA GCT AGC AAG ATC AAC GAT GAT GAC TCC TTC ACC ACC TTT TTC AGC      198
Gln Ala Ser Lys Ile Asn Asp Asp Asp Ser Phe Thr Thr Phe Phe Ser
                10                  15                  20

GAG ACT GGC ACT TCT CTG CTG ATG GAA CGC CTC TSC CTG GAT TAT GGC      246
Glu Thr Gly Thr Ser Leu Leu Met Glu Arg Leu Xaa Leu Asp Tyr Gly
            25                  30                  35

AAG AAA                                                               252
Lys Lys
    40
```

(2) INFORMATION FOR SEQ ID NO: 246:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 172 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 82..168
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                            region 107..193
                            id AA088577
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 31..71
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                            region 53..93
                            id AA088577
                            est

    (ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 31..168
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 24..161
                                id R16448
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 53..168
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 23..138
                                id AA094092
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 31..163
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 24..156
                                id R18030
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 60..168
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 43..151
                                id W00599
                                est

   (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 29..70
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 95
                                region 13..54
                                id W00599
                                est

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 35..109
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.2
                                seq LDLLRGLPRVSLA/NL

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:


AAGGGCGCCC TTGAAAGTTC TTGGATCTGC GGGT ATG GCC GGT CCC TTG CAG GGC   55
                                       Met Ala Gly Pro Leu Gln Gly
                                       -25                     -20

GGT GGG GCC CGG GCC CTG GAC CTA CTC CGG GGC CTG CCG CGT GTG AGC    103
Gly Gly Ala Arg Ala Leu Asp Leu Leu Arg Gly Leu Pro Arg Val Ser
          -15                 -10                 -5
```

```
CTG GCC AAC TTA AAG CCG AAT CCC GGC TCC AAG AAA CCG GAG AGA AGA      151
Leu Ala Asn Leu Lys Pro Asn Pro Gly Ser Lys Lys Pro Glu Arg Arg
        1                   5                   10

CCA AGA GGT CGG AGA AGG TGG                                          172
Pro Arg Gly Arg Arg Arg Trp
 15                  20
```

(2) INFORMATION FOR SEQ ID NO: 247:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 359 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 52..360
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                            region 1..309
                            id HSC1ED081
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 171..316
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                            region 146..291
                            id AA143136
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 31..165
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                            region 6..140
                            id AA143136
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 310..341
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                            region 286..317
                            id AA143136
                            est

```
        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 176..282
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 99
                                     region 77..183
                                     id N75929
                                     est


        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 102..165
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 98
                                     region 3..66
                                     id N75929
                                     est


        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 156..230
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 4.2
                                     seq MFAASXLAMCAGA/EV


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:


ATTTTGGGTC CGGCCTGCTC GCMGTCCGCT CCGTCCGCCC TTAGACCTGT TGCCCAGCAT    60

CCCTGCAGTT CGCGGWACAG TCTCTATTAG AGCGCGTGTA TAGAGGCAGA KAGGAGTGAA   120

GTCCACAGTT CCTCTCCTCC TAGAGCCTGC CGACC ATG CCC GCG GGC GTG CCC      173
                                        Met Pro Ala Gly Val Pro
                                        -25             -20

ATG TCC ACC TAC CTG AAA ATG TTC GCA GCC AGT MTC CTG GCC ATG TGC    221
Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Xaa Leu Ala Met Cys
            -15             -10                         -5

GCA GGG GCA GAA GTG GTG CAC AGG TAC TAC CGA CCG GAC CTG ACA ATA    269
Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
            1               5                   10

CCT GAA ATT CCA CCA AAG CGT GGA GAA CTC AAA ACG GAG CTT TTG GGA    317
Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
    15              20                  25

CTG AAA GAA AGA AAA CAC AAA CCT CAA GTT TCT CAA CAG GAG            359
Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu
30              35                  40




(2) INFORMATION FOR SEQ ID NO: 248:


        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 284 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR
```

```
(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Homo Sapiens
     (F) TISSUE TYPE: Brain

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 10..280
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                             region 17..287
                             id AA082102
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 72..224
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                             region 30..182
                             id R10417
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 221..280
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 180..239
                             id R10417
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 47..280
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 99
                             region 2..235
                             id W73318
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 42..224
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 1..183
                             id R08733
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 237..269
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 93
                             region 198..230
                             id R08733
                             est
```

```
    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 39..110
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:   score 4.2
                                  seq SLPALALSLRASP/RX


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:


AAGTGCGTGC GCGGCGACTG CGACGGGCAG TGGCAGTC ATG GCG GTT CAG TGC GTG       56
                                           Met Ala Val Gln Cys Val
                                                              -20


AGG TTG GCG CGG CGC AGT CTT CCT GCT TTG GCG TTG TCT CTC AGG GCA        104
Arg Leu Ala Arg Arg Ser Leu Pro Ala Leu Ala Leu Ser Leu Arg Ala
              -15             -10             -5


TCT CCC CGG KTG TTG TGC ACA GCC ACG AAA CAA AAG AAC AGT GGC CAG        152
Ser Pro Arg Xaa Leu Cys Thr Ala Thr Lys Gln Lys Asn Ser Gly Gln
         1            5               10


AAC CTG GAA GAG GAC ATG GGT CAG AGT GAA CAG AAG GCA GAT CCT CCT        200
Asn Leu Glu Glu Asp Met Gly Gln Ser Glu Gln Lys Ala Asp Pro Pro
 15              20              25                 30


GCT ACA GAG AAG ACC CTC CTG GAA GAG AAG GTC AAG TTG GAG GAA CAG        248
Ala Thr Glu Lys Thr Leu Leu Glu Glu Lys Val Lys Leu Glu Glu Gln
             35              40              45


CTG AAG GAG ACT GTG GAA AAA TAT AAA CGA GCG AGG                        284
Leu Lys Glu Thr Val Glu Lys Tyr Lys Arg Ala Arg
         50              55



(2) INFORMATION FOR SEQ ID NO: 249:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 307 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: complement(34..74)
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 92
                                  region 271..311
                                  id T05270
                                  est

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
```

        (B) LOCATION: 182..292
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.2
                                seq RLMHHYLSTPTSA/RP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

AAAGGCTGCC CTGTGGCACC ACAATCTAAG CTCAGGGCAT AAAACCCCTT GTGGCTTTGA   60

TGGAATCCAG GGCTCAGACC ATAAAACCCC TCGTGGCCTT TTGAATGTGC ACCGACTTGC   120

TGGCTCCTTG CTTCTTGCTC TCCCAGAATC GTAAATTGAT TGTATCTTGA GTTGGAAGAA   180

C ATG TTC TCC ATT ATC TCA CGT AGC AGA GCA TGT TCC ATG TAC TTC AAA   229
  Met Phe Ser Ile Ile Ser Arg Ser Arg Ala Cys Ser Met Tyr Phe Lys
        -35   -30   -25

GAA AAT GCT AAA CCG TCA CAG CTA CGC TTG ATG CAC CAC TAC CTT TCT   277
Glu Asn Ala Lys Pro Ser Gln Leu Arg Leu Met His His Tyr Leu Ser
    -20   -15   -10

ACC CCC ACA TCC GCA CGT CCT CAC CAC CTG   307
Thr Pro Thr Ser Ala Arg Pro His His Leu
 -5   1   5

(2) INFORMATION FOR SEQ ID NO: 250:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 212 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(1..209)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                    region 125..333
                                    id H40205
                                    est

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(80..209)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 96
                                    region 131..260
                                    id H03462
                                    est

        (ix) FEATURE:

          (A) NAME/KEY: other
          (B) LOCATION: complement(52..90)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 97
                                  region 251..289
                                  id H03462
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(17..54)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 97
                                  region 288..325
                                  id H03462
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(17..209)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 95
                                  region 130..322
                                  id R05443
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(128..209)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 143..224
                                  id T52770
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(80..128)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 225..273
                                  id T52770
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(43..74)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 96
                                  region 281..312
                                  id T52770
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(57..209)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 98
                                  region 143..295
                                  id AA037595
                                  est

```
    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: 108..155
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 4.1
                                 seq LLPATSLAGPVLS/TL


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:


ACTTCTTGTG GACTCACCAA GAGAAACAAA AGGAAGCCTG CACCATTGTA GCCCTGAACT    60

CTTTTCTGGG CACCTGAATC CCAGGAACCC TCAATGAGGT CTTCAAG ATG AAG AGA    116
                                                     Met Lys Arg
                                                     -15

CTG CTG CCA GCT ACC AGC CTG GCT GGC CCT GTC CTG TCC ACC CTC ATT    164
Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser Thr Leu Ile
        -10                 -5                  1

GCC CCA ACT CCC ATG TTG TTT TGT GAA GAT AAA AGC TGG GAT CCT GGG    212
Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp Asp Pro Gly
    5                10                  15
```

```
(2) INFORMATION FOR SEQ ID NO: 251:

    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 357 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 108..308
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 95
                                 region 116..316
                                 id HSC2TH021
                                 est

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 16..99
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 97
                                 region 24..107
                                 id HSC2TH021
                                 est

    (ix) FEATURE:
         (A) NAME/KEY: other
```

        (B) LOCATION: 30..92
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                                region 72..134
                                id W54529
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 119..352
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                                region 23..256
                                id R59681
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 64..273
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4
                                seq IAVLYLHLYDVFG/DP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

AACTGTCCGG GGCTGCGGGG CTTGCTTCCG GCGTCATGGC TCAAAGGGCC TTCCCGAATC   60

CTT ATG CTG ATT ATA ACA AAT CCC TGG CCG AAG TAC TTT GAT GCT GCC   108
    Met Leu Ile Ile Thr Asn Pro Trp Pro Lys Tyr Phe Asp Ala Ala
    -70   -65   -60

GGG AGG CTG ACT CCT GAG TTC TCA CAA CGC TTG ACC AAT AAG ATT CGG   156
Gly Arg Leu Thr Pro Glu Phe Ser Gln Arg Leu Thr Asn Lys Ile Arg
-55   -50   -45   -40

GAG CTT CTT CAG CAA ATG GAG AGA GGC CTG AAA TCA GCA GAC CBB MSG   204
Glu Leu Leu Gln Gln Met Glu Arg Gly Leu Lys Ser Ala Asp Xaa Xaa
                -35   -30   -25

GAT GGC ACC GGT TAC ACT GGC TGG GCA GGT ATT GCT GTG CTT TAC TTA   252
Asp Gly Thr Gly Tyr Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu
        -20   -15   -10

CAT CTT TAT GAT GTA TTT GGG GAC CCT GCC TAC CTA CAG TTA GCA CAT   300
His Leu Tyr Asp Val Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His
        -5   1   5

GGC TAT GTA AAG CAA AGT CTG AAC TGC TTA ACC AAG CGC TCC ATC ACC   348
Gly Tyr Val Lys Gln Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr
10   15   20   25

TTC CAA GGG   357
Phe Gln Gly

(2) INFORMATION FOR SEQ ID NO: 252:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 414 base pairs

```
        (B)  TYPE: NUCLEIC ACID
        (C)  STRANDEDNESS: DOUBLE
        (D)  TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: cDNA

   (vi) ORIGINAL SOURCE:
        (A)  ORGANISM: Homo Sapiens
        (F)  TISSUE TYPE: Brain

   (ix) FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 11..238
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 100
                                 region 1..228
                                 id R26618
                                 est

   (ix) FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 283..397
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 98
                                 region 96..210
                                 id HUM528H09B
                                 est

   (ix) FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 202..282
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 98
                                 region 16..96
                                 id HUM528H09B
                                 est

   (ix) FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 283..411
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 96
                                 region 110..238
                                 id C18739
                                 est

   (ix) FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 202..282
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 98
                                 region 30..110
                                 id C18739
                                 est

   (ix) FEATURE:
        (A)  NAME/KEY: other
        (B)  LOCATION: 235..411
        (C)  IDENTIFICATION METHOD: blastn
        (D)  OTHER INFORMATION:  identity 97
                                 region 1..177
```

                                    id R17985
                                    est

        (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: complement(2..70)
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION: identity 97
                                    region 9..77
                                    id R40947
                                    est

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 274..336
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 3.9
                                    seq AWLAQGSSSAGWG/LE

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

ATCAATTTTK TGAATAGTTT CCATTTCAAA TATCTTGTTC TACTTGGTTC ATAAAATAGT   60

GGTTTTCAAA CTGTAGAGCT CTGGACTTCT CACTTCTAGG GCAGAGGGAG CCTGAACAAG   120

TGAGGCTCTG GGTTCCCCAT TCCTAATTAA ACCAATGGAA AGAAGGGGTC TAATAACAAA   180

CTACAGCAAC ACATTTTTCA TTTCAGCTTC ACTGCTGTAT CTCCCAGTCT AACCCTAGCA   240

TCCAGAAGTG GCACAAAACC CCTCTGCTGG CTC ATG TGT GCA ACT GAG ACT GTC   294
                                   Met Cys Ala Thr Glu Thr Val
                                   -20   -15

AGA GCA TGG CTA GCT CAG GGG TCC AGC TCT GCA GGG TGG GGG CTA GAG   342
Arg Ala Trp Leu Ala Gln Gly Ser Ser Ser Ala Gly Trp Gly Leu Glu
        -10   -5   1

AGG AAG CAG GGA GTA TCT GCA CAC AGG ATG CCC GCG CTC AGG TGG TTG   390
Arg Lys Gln Gly Val Ser Ala His Arg Met Pro Ala Leu Arg Trp Leu
        5   10   15

CAG AAG TCA GTG CCA GGA BCC ATG   414
Gln Lys Ser Val Pro Gly Xaa Met
    20   25

(2) INFORMATION FOR SEQ ID NO: 253:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 189 base pairs
             (B) TYPE: NUCLEIC ACID
             (C) STRANDEDNESS: DOUBLE
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 124..153
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 25..54
                             id N91869
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 124..153
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 5..34
                             id H53427
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 124..153
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 19..48
                             id H88369
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 124..153
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 26..55
                             id T79771
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 124..153
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 29..58
                             id H41152
                             est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 46..183
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 3.9
                             seq AAAFCLKXXGANT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:


AGAATTTCTC CCACTCTTCG AGCCTACAGC AGACATGTTA GGAGA ATG CTG CTG CTT    57
                                                  Met Leu Leu Leu
                                                      -45

GCA ACA CAC CCA GAG ACG GTG GGG CAG GTG ACA CTG CGT GTG TRC CCG    105
```

```
Ala Thr His Pro Glu Thr Val Gly Gln Val Thr Leu Arg Val Xaa Pro
    -40                 -35                 -30

GTG TCT CTG GAA GTG TCT ATA CAG ATG TGT GCT GCT GCT GCT GCT GCT     153
Val Ser Leu Glu Val Ser Ile Gln Met Cys Ala Ala Ala Ala Ala Ala
    -25                 -20             -15

TTC TGC CTT AAA ATK WCT GGA GCC AAC ACC CAC CCA                     189
Phe Cys Leu Lys Xaa Xaa Gly Ala Asn Thr His Pro
-10              -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 254:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 300 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 149..232
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 96
                              region 91..174
                              id AA081517
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 224..297
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97
                              region 165..238
                              id AA081517
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 90..141
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 98
                              region 34..85
                              id AA081517
                              est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 76..141
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 93
                              region 20..85
                              id N53273

                                               est

        (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 149..193
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 97
                                      region 91..135
                                      id N53273
                                      est

        (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: complement(237..297)
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 100
                                      region 172..232
                                      id H14293
                                      est

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: 43..234
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 3.9
                                      seq GLGGAQLQGGAXG/RG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AGTCTCTGGG CGCGGCCATG TTGGAGGSTC CGGGCCCGAG TG ATG GCT GCG AGC   54
                                               Met Ala Ala Ser

TCA GCA ACC CCA GCG CCS ASC RGA AGT CAG CGG TGC GGG GCA GAT GCT   102
Ser Ala Thr Pro Ala Pro Xaa Xaa Ser Gln Arg Cys Gly Ala Asp Ala
-60   -55   -50   -45

GGA AGT GCA GCC AGG ATT GTA TTT CGG TGG GGC CGC GGC CGT CGC GGA   150
Gly Ser Ala Ala Arg Ile Val Phe Arg Trp Gly Arg Gly Arg Arg Gly
                -40   -35   -30

GCC AGA TCA CCT GAG GGA AGC GGG CAT CAC GGC CGT GCT AAC AGT GGA   198
Ala Arg Ser Pro Glu Gly Ser Gly His His Gly Arg Ala Asn Ser Gly
            -25   -20   -15

CTC GGA GGA GCC CAG CTT CAA GGC GGG GCC TRG GGT CGA GGA TCT ATG   246
Leu Gly Gly Ala Gln Leu Gln Gly Gly Ala Xaa Gly Arg Gly Ser Met
            -10   -5   1

GCG CCT CTT CGT GCC AGC GCT GGA CAA ACC CGA GAC GGA CCT ACT CAG   294
Ala Pro Leu Arg Ala Ser Ala Gly Gln Thr Arg Asp Gly Pro Thr Gln
5   10   15   20

CCA GGG   300
Pro Gly

(2) INFORMATION FOR SEQ ID NO: 255:

        (i) SEQUENCE CHARACTERISTICS:

```
        (A) LENGTH: 151 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 13..150
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 1..138
                                id T36282
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 46..150
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 1..105
                                id T08090
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 46..150
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 1..105
                                id T08091
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 72..150
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 1..79
                                id H56620
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 80..150
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 1..71
                                id AA027983
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 2..52
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 3.9
```

seq PLAGLAAAALGRA/PP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

A ATG CTG CGG CGC CCG CTG GCC GGG CTG GCT GCG GCC GCC CTG GGC CGG   49
   Met Leu Arg Arg Pro Leu Ala Gly Leu Ala Ala Ala Ala Leu Gly Arg
       -15   -10   -5

GCC CCA CCG GAC GGC TTG CTC TGC TCT TTA CCT GGG GTT GCT GTC GAG   97
Ala Pro Pro Asp Gly Leu Leu Cys Ser Leu Pro Gly Val Ala Val Glu
    1   5   10   15

GAC CCT GTG CAA GAC TCG GCC GGT TTT TCT TTC TCC CTG ATG GAC AGA   145
Asp Pro Val Gln Asp Ser Ala Gly Phe Ser Phe Ser Leu Met Asp Arg
       20   25   30

CCC AAG   151
Pro Lys

(2) INFORMATION FOR SEQ ID NO: 256:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 217 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 3..214
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                     region 14..225
                                     id H08058
                                     est

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 2..91
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 100
                                     region 10..99
                                     id R11727
                                     est

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 59..109
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.8
                                     seq GFVAALVAGGVAG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```
AGACGTGATC CGCTTCTGCT CCGGCTTGGA TTGTAGCCTT GACGAGGTCT GAGCGACC          58

ATG GAC CGG CCG GGG TTC GTG GCA GCG CTG GTG GCT GGT GGG GTA GCA         106
Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
        -15            -10             -5

GGT GTT TCT GTT GAC TTG ATA TTA TTT CCT CTG GAT ACC ATT AAA ACC        154
Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1               5                  10                  15

AGG CTG CAG AGT CCC CAA GGA TTT AGT AAG GCT GGT GGT TTT CAT GGA        202
Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
             20              25                  30

ATA TAT GCT AGC TGG                                                     217
Ile Tyr Ala Ser Trp
         35
```

(2) INFORMATION FOR SEQ ID NO: 257:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 158 base pairs
                (B) TYPE: NUCLEIC ACID
                (C) STRANDEDNESS: DOUBLE
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 39..155
                (C) IDENTIFICATION METHOD: blastn
                (D) OTHER INFORMATION: identity 98
                                         region 1..117
                                         id C01598
                                         est

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 9..71
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 3.8
                                         seq SMDLLTLLFQRRS/HQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```
AATCAAGT ATG ATT GTT TGG TTT GAG GGT ATT TCC ATG GAT CTC CTT ACA        50
         Met Ile Val Trp Phe Glu Gly Ile Ser Met Asp Leu Leu Thr
          -20              -15             -10

CTG CTA TTC CAG AGG AGA AGC CAC CAG GTC ACT CAA CTC TTA GTA TCA        98
```

```
Leu Leu Phe Gln Arg Arg Ser His Gln Val Thr Gln Leu Leu Val Ser
        -5                   1                   5
```

```
TCT ACT GGA AAC TGG CTA AGA CAG TAT TTA TGT GCT TCT CTC ACA ATA    146
Ser Thr Gly Asn Trp Leu Arg Gln Tyr Leu Cys Ala Ser Leu Thr Ile
 10                  15                  20                  25
```

```
GCA GGA AGA AGG                                                    158
Ala Gly Arg Arg
```

(2) INFORMATION FOR SEQ ID NO: 258:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 292 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(192..269)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                            region 354..431
                            id N70088
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(222..262)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 95
                            region 399..439
                            id H30254
                            est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 143..202
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.8
                            seq ALDALMFPARRRA/AV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AAGCGGCTGT CCTCCCTCGC TTTTGGAGCT CCGACCTCAG CTTCGCCTGC GAGCTGGGTT    60

GTGTAAAGGC TGGTCATTTT GGGGCGCTTA GGGGTGGGTG CCGGGGGGCG CGCTTTCCCT   120

CGTGAAGGTC GCTCCAGGAG TC ATG CGT ACA TTC GTT CAT TTT GCT CTG GAC   172
                         Met Arg Thr Phe Val His Phe Ala Leu Asp
                         -20                 -15
```

```
GCA CTG ATG TTC CCG GCT CGC CGC CGT GCC GCA GTC ACG AGG CTC TCC    220
Ala Leu Met Phe Pro Ala Arg Arg Arg Ala Ala Val Thr Arg Leu Ser
-10        -5              1              5

GAA CGC CTT TCA CTG TGT TTC TGT TTA CAT TCG CGT CTG CAA GAC CCG    268
Glu Arg Leu Ser Leu Cys Phe Cys Leu His Ser Arg Leu Gln Asp Pro
          10              15              20

GCG GCG CGA CCG AGG CCC TCT TGG                                     292
Ala Ala Arg Pro Arg Pro Ser Trp
          25              30
```

(2) INFORMATION FOR SEQ ID NO: 259:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 338 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 131..273
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 92
                            region 120..262
                            id R10063
                            ·est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 35..101
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                            region 26..92
                            id R10063
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 103..149
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 100
                            region 93..139
                            id R10063
                            est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 275..312
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION: identity 97

                                              region 266..303
                                              id R10063
                                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 131..273
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 92
                              region 130..272
                              id R12045
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 35..100
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 100
                              region 36..101
                              id R12045
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 103..149
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 100
                              region 103..149
                              id R12045
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 3..35
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 96
                              region 5..37
                              id R12045
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 131..273
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 92
                              region 125..267
                              id R12117
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 5..100
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 98
                              region 1..96
                              id R12117
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 103..149

```
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 100
                                 region 98..144
                                 id R12117
                                 est


(ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 131..273
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 92
                                 region 102..244
                                 id T79499
                                 est


(ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 28..102
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 93
                                 region 1..75
                                 id T79499
                                 est


(ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 104..149
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 97
                                 region 76..121
                                 id T79499
                                 est


(ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 275..312
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 97
                                 region 248..285
                                 id T79499
                                 est


(ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 109..178
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 95
                                 region 109..178
                                 id H17371
                                 est


(ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 275..332
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:  identity 100
                                 region 283..340
                                 id H17371
                                 est


(ix) FEATURE:
```

```
        (A) NAME/KEY: other
        (B) LOCATION: 44..106
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 95
                                region 42..104
                                id H17371
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 42..224
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 3.8
                                seq LVMTFLFRNGSLQ/EK

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:
```

```
AGCTTACAGT TCCTAACCCC GACCCTGCGC GCASCCGCAC T ATG GCA GCC CCG CCG    56
                                              Met Ala Ala Pro Pro
                                              -60


CAG CTA AGG GCT CTG CTC GTA GTC GTC AAC GCA CTG CTG CGC AAG CGC     104
Gln Leu Arg Ala Leu Leu Val Val Val Asn Ala Leu Leu Arg Lys Arg
  -55              -50               -45


CGC TAC CAC GCT GCG TTG GCC GTG CTT AAG GGC TTC CGG AAC GGG GCT     152
Arg Tyr His Ala Ala Leu Ala Val Leu Lys Gly Phe Arg Asn Gly Ala
-40              -35               -30                   -25


GTC TAT GGA GCC AAA ATC CGG GCC CCT CAC GCG CTG GTC ATG ACC TTT     200
Val Tyr Gly Ala Lys Ile Arg Ala Pro His Ala Leu Val Met Thr Phe
             -20               -15               -10


CTC TTC CGG AAT GGC AGC CTC CAG GAG AAG CTG TGG GCC ATA CTG CAG     248
Leu Phe Arg Asn Gly Ser Leu Gln Glu Lys Leu Trp Ala Ile Leu Gln
             -5                1                5


GCC ACA TAT ATC CAC TCC TGG AAC CTG GCA CGG TTT GTG TTC ACC TAC     296
Ala Thr Tyr Ile His Ser Trp Asn Leu Ala Arg Phe Val Phe Thr Tyr
    10               15                20


AAG GGT CTC CGT GCC CTG CAG TCC TAC ATA CAA GGC CCT GGG             338
Lys Gly Leu Arg Ala Leu Gln Ser Tyr Ile Gln Gly Pro Gly
25               30               35
```

(2) INFORMATION FOR SEQ ID NO: 260:

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 364 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 44..158
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 99
                             region 208..322
                             id AA017601
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 287..334
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 451..498
                             id AA017601
                             est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 128..181
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 3.8
                             seq GXALGLLPSLAKA/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:
```

```
ACCCAGCTCC CGGAAGTGCG CCCGGAGCCG GCGCCGCGGG CCGAGTGTCC TGGTGAAGAC    60

CTAGTTCTTG CCGGAGACAA TTCCACTGCA GAAGCACTTT ACTTAAAAGG ACTTGCCAGG   120

CTGGACA ATG CCC GTT GAC TTG GGG CAD GCC CTA GGC CTG CTG CCA TCG     169
        Met Pro Val Asp Leu Gly Xaa Ala Leu Gly Leu Leu Pro Ser
                    -15                 -10               .-5

CTG GCG AAG GCC GAG GAC TCC CAG TTC TCA GAA TCA GAT GCT GCC CTT     217
Leu Ala Lys Ala Glu Asp Ser Gln Phe Ser Glu Ser Asp Ala Ala Leu
             1               5                10

CAA GAG GAA CTC TCC AGC CCT GAG ACC GCA CGC CAG CTT TTC AGG CAG     265
Gln Glu Glu Leu Ser Ser Pro Glu Thr Ala Arg Gln Leu Phe Arg Gln
         15               20               25

TTC CGT TAC CAG GTG ATG TCT GGG CCT CAT GAG ACC TTG AAG CDA CTT     313
Phe Arg Tyr Gln Val Met Ser Gly Pro His Glu Thr Leu Lys Xaa Leu
     30               35               40

CGG AAG CTC TGT TTC CAG TGG CTA CAG CCA GAG GTT CAC ACC AAA GAG     361
Arg Lys Leu Cys Phe Gln Trp Leu Gln Pro Glu Val His Thr Lys Glu
 45               50               55               60

GGG                                                                  364
Gly
```

```
(2) INFORMATION FOR SEQ ID NO: 261:

    (i) SEQUENCE CHARACTERISTICS:
```

          (A) LENGTH: 433 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(324..433)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 100
                                  region 253..362
                                  id H93008
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(200..267)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 92
                                  region 423..490
                                  id H93008
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(159..205)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 93
                                  region 484..530
                                  id H93008
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(116..162)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 91
                                  region 526..572
                                  id H93008
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(259..299)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 97
                                  region 390..430
                                  id H93008
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(52..83)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION: identity 90

```
                                        region 602..633
                                        id H93008
                                        est
```

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 67..243
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 100
                                  region 1..177
                                  id AA146840
                                  est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 332..417
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 100
                                  region 269..354
                                  id AA146840
                                  est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 242..299
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 100
                                  region 177..234
                                  id AA146840
                                  est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 299..334
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 100
                                  region 235..270
                                  id AA146840
                                  est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 85..299
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 99
                                  region 1..215
                                  id AA036893
                                  est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 299..412
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                                  region 216..329
                                  id AA036893
                                  est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 98..243
```

```
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 98
                                     region 1..146
                                     id T49176
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 242..299
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 146..203
                                     id T49176
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 344..396
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 98
                                     region 250..302
                                     id T49176
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 299..349
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 96
                                     region 204..254
                                     id T49176
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 19..243
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 1..225
                                     id H01262
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: other
             (B) LOCATION: 242..296
             (C) IDENTIFICATION METHOD: blastn
             (D) OTHER INFORMATION:  identity 100
                                     region 225..279
                                     id H01262
                                     est

     (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: 17..232
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 3.8
                                     seq LMGLALAVYKCQS/MG

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:
```

ACTCAAACAG ATTCCC ATG AAT CTC TTC ATC ATG TAC ATG GCA GGC AAT ACT   52
                  Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
                      -70   -65

ATC TCC ATC TTC CCT ACT ATG ATG GTG TGT ATG ATG GCC TGG CGA CCC   100
Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro
-60   -55   -50   -45

ATT CAG GCA CTT ATG GCC ATT TCA GCC ACT TTC AAG ATG TTA GAA AGT   148
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
                -40   -35   -30

TCA AGC CAG AAG TTT CTT CAG GGT TTG GTC TAT CTC ATT GGG AAC CTG   196
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
            -25   -20   -15

ATG GGT TTG GCA TTG GCT GTT TAC AAG TGC CAG TCC ATG GGA CTG TTA   244
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
        -10   -5   1

CCT ACA CAT GCA TCG GAT TGG TTA GCC TTC ATT GAG CCC CCT GAG AGA   292
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
5   10   15   20

ATG GAG TCA GTG GTG GAG GAC TGC TTT TGT GAA CAT GAG AAA GCA GCG   340
Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
            25   30   35

CCT GGT CCC TAT GTA TTT GGG TCT TAT TTA CAT CCT TCT TTA AGC CCA   388
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
            40   45   50

GTG GCT CCT CAG CAT ACT CTT AAA CTA ATC ACT TAT GTT AAA AAG   433
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys
            55   60   65

    (2) INFORMATION FOR SEQ ID NO: 262:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 370 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 2..250
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION: identity 99
                                  region 14..262
                                  id N33874
                                  est

```
(ix). FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: 78..270
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 98
                               region 1..193
                               id H01141
                               est

(ix) FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: 283..349
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 97
                               region 207..273
                               id H01141
                               est

(ix) FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: 284..366
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 92
                               region 320..402
                               id AA023741
                               est

(ix) FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: 74..270
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 100
                               region 2..198
                               id R27699
                               est

(ix) FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: 320..349
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 93
                               region 253..282
                               id R27699
                               est

(ix) FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: complement(320..366)
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 97
                               region 282..328
                               id N33481
                               est

(ix) FEATURE:
       (A) NAME/KEY: other
       (B) LOCATION: complement(283..322)
       (C) IDENTIFICATION METHOD: blastn
       (D) OTHER INFORMATION:  identity 100
                               region 327..366
                               id N33481
```

est

    (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(235..270)
            (C) IDENTIFICATION METHOD: blastn
          · (D) OTHER INFORMATION: identity 97
                                    region 379..414
                                    id N33481
                                    est

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 65..217
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.8
                                    seq NVLFVAGLAFVIG/LE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

ACGACTCAGC TTCCCACCCT GGGCTTTCCG AGGTGCTTTC GCCGCTGTCC CCACCACTGC   60

AGCC ATG ATC TCC TTA ACG GAC ACG CAG AAA ATT GGA ATG GGA TTA ACA   109
     Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr
     -50   -45   -40

GGA TTT GGA GTG TTT TTC CTG TTC TTT GGA ATG ATT CTC TTT TTT GAC   157
Gly Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp
-35   -30   -25

AAA GCA CTA CTG GCT ATT GGA AAT GTT TTA TTT GTA GCC GGC TTG GCT   205
Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala
-20   -15   -10   -5

TTT GTA ATT GGT TTA GAA AGA ACA TTC AGA TTC TTC TTC CAA AAA CAT   253
Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His
            1   5   10

AAA ATG AAA GCT ACA GGT TTT TTT CTG GGT GGT GTA TTT GTA GTC CTT   301
Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu
        15   20   25

ATT GGT TGG CCT TTG ATA GGC ATG ATC TTC GAA ATT TAT GGA TTT TTT   349
Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe
    30   35   40

CTC TTG TTC AGG GGC TTA GGG   370
Leu Leu Phe Arg Gly Leu Gly
·45   50

(2) INFORMATION FOR SEQ ID NO: 263:

    (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 249 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 112..249
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
                            region 153..290
                            id AA010288
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 112..218
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 96
                            region 101..207
                            id R26319
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 208..247
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 92
                            region 198..237
                            id R26319
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 110..249
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 95
                            region 24..163
                            id W69087
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: 112..247
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 98
                            region 103..238
                            id H01791
                            est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(112..217)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 98
                            region 287..392
                            id AA146617
                            est

(ix) FEATURE:

          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 91..189
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 3.6
                                  seq LAVFQMLKSMCAG/QR

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

AAAAAAGCGA AGGCCGGCCG GGCGGGGAAG GGAAATGGCG AGGCAGGAGT GCGGGGGAGG   60

GAGTGGTCCT TAGCTGAATG CGCCTGCGTT ATG GCG GCC TCC GGC GCC CCA AGG   114
                                  Met Ala Ala Ser Gly Ala Pro Arg
                                                              -30

ATC CTG GTG GAC CTG CTG AAG CTG ASC GTG GCC CCC CTC GCC GTC TTC   162
Ile Leu Val Asp Leu Leu Lys Leu Xaa Val Ala Pro Leu Ala Val Phe
-25   -20   -15   -10

CAG ATG CTC AAG TCC ATG TGT GCC GGG CAG AGG CTA GCG AGC GAG CCC   210
Gln Met Leu Lys Ser Met Cys Ala Gly Gln Arg Leu Ala Ser Glu Pro
              -5   1   5

CAG GAC CCT GCG GCC GTG TCT CTG CCC ACG TCG AGC GGG   249
Gln Asp Pro Ala Ala Val Ser Leu Pro Thr Ser Ser Gly
         10   15   20

     (2) INFORMATION FOR SEQ ID NO: 264:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 324 base pairs
              (B) TYPE: NUCLEIC ACID
              (C) STRANDEDNESS: DOUBLE
              (D) TOPOLOGY: LINEAR

          (ii) MOLECULE TYPE: CDNA

          (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

          (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 52..178
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 98
                                      region 68..194
                                      id W51974
                                      est

          (ix) FEATURE:
              (A) NAME/KEY: other
              (B) LOCATION: 173..253
              (C) IDENTIFICATION METHOD: blastn
              (D) OTHER INFORMATION: identity 98
                                      region 190..270
                                      id W51974
                                      est

```
(ix). FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 49..126
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 3.6
                              seq ARSLLQFLRLVGQ/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:


AAGGAGCTTC GCCGCGGCCT GCTCCGCCCA GCCGGGGTCG GTGGCCGC ATG GCT TCG      57
                                                     Met Ala Ser
                                                         -25

GTC TCC TCT GCG ACC TTC TCG GGC CAC GGG GCT CGG TCC CTA CTG CAG     105
Val Ser Ser Ala Thr Phe Ser Gly His Gly Ala Arg Ser Leu Leu Gln
            -20             -15             .            -10

TTC CTG CGG CTG GTA GGG CAG CTC AAG AGA GTC CCA CGA ACT GGC TGG     153
Phe Leu Arg Leu Val Gly Gln Leu Lys Arg Val Pro Arg Thr Gly Trp
        -5                   1               5

GTA TAC AGA AAT GTC CAG AGG CCG GAG AGC GTT TCA GAT CAC ATG TAC     201
Val Tyr Arg Asn Val Gln Arg Pro Glu Ser Val Ser Asp His Met Tyr
10              15              20              25

CGG ATG GCA GTT ATG GCT ATG GTG ATC AAA GAT GAC CGT CTT AAC AAA     249
Arg Met Ala Val Met Ala Met Val Ile Lys Asp Asp Arg Leu Asn Lys
            30              35              40

GAC CGA TGT GTA CGC CTA GCC CTG GTT CAT GAT ATG GCA GAA TGC ATC     297
Asp Arg Cys Val Arg Leu Ala Leu Val His Asp Met Ala Glu Cys Ile
            45              50              55

GTT GGG GAC ATA GCA CCA GCA GAT GGG                                  324
Val Gly Asp Ile Ala Pro Ala Asp Gly
        60              65


(2) INFORMATION FOR SEQ ID NO: 265:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 157 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA .

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(2..156)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 72..226
                                id AA134487
```

est

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(43..156)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 98
                              region 73..186
                              id T23528
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(6..156)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:   identity 96
                              region 69..219
                              id R50519
                              est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 86..133
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:   score 3.6
                              seq LAVLLVLFTLNIL/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:


ACTGTATAAT RTGTGTATAT KAAAATGTAA TTGATTTCAG YYGAAAGTAT TTTAAAGCTG    60


ATAAATAGCA TTAGGGTTCT TTGCA ATG TGG TAT CTA GCT GTA TTA TTG GTT    112
                            Met Trp Tyr Leu Ala Val Leu Leu Val
                            -15                 -10

TTA TTT ACT TTA AAC ATT TTG AAA AGC TTA TAC TGG CAG CCT GGG        157
Leu Phe Thr Leu Asn Ile Leu Lys Ser Leu Tyr Trp Gln Pro Gly
    -5                   1             5



(2) INFORMATION FOR SEQ ID NO: 266:

    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 370 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 41..79
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 92
```

```
                              region 80..118
                              id T06923
                              est
```

```
     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 197..322
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 3.5
                              seq INSLLEXSSLSRC/LE

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:


ACATAAAGGA CASACGAGTC CTAATTGACA ACATCTAGTC TTTCTGGATG TTAAAGAGGT   60

TGCCAGTGTA TGACAAAAGT AGAGTTAGTA AACTAATATA TTTTGTACAT TTTGTTTTAC  120

AAGTCCTAGG AAAGATTGTC TTCTGAAAAT TTGATGTCTT CTGGGTTGAW GGAGATGGGA  180

AGGGTTCTAG GCCAGA ATG TTC ACA TTT GGA AGA CTC TTT CAA ATT ATA ACT  232
                  Met Phe Thr Phe Gly Arg Leu Phe Gln Ile Ile Thr
                  -40                      -35

GTT GTT ACA TGT TTG CAG TTT ATT CAA GAC TGC TGT ATA CAT AGT AGA   280
Val Val Thr Cys Leu Gln Phe Ile Gln Asp Cys Cys Ile His Ser Arg
-30               -25                 -20                     -15

CAA ATT AAC TCC TTA CTT GAR RCA TCT AGT CTA TCT AGA TGT TTA GAA   328
Gln Ile Asn Ser Leu Leu Glu Xaa Ser Ser Leu Ser Arg Cys Leu Glu
              -10                 -5                        1

GTG CCG ATG TAT GTY AAA TGT ATA GGT AGT AAA ATA CCA CTT           370
Val Pro Met Tyr Val Lys Cys Ile Gly Ser Lys Ile Pro Leu
         5                10                15
```

```
(2) INFORMATION FOR SEQ ID NO: 267:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 301 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: CDNA

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 53..297
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 96
                              region 31..275
                              id HUM414A03B
                              est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 22..51
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 100
                            region 1..30
                            id HUM414A03B
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 106..256
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 99
                            region 84..234
                            id H83476
                            est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 48..105
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION: identity 96
                            region 27..84
                            id H83476
                            est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 116..268
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 3.5
                            seq VGTLCQLDWWIWG/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:


AAAATCAAGG CAGGGGATGG AGGCAAGTGG GGGTCGCGCC TGGAGCGGAG CRTCGGCCTC    60

CGGAGCCGCA GCTGCAGCCC TGTATTGAGC TGAGATGGCT CGAGCCTAAC ATTCC ATG    118
                                                                 Met

ATC CAG GAT CGT GAC AGA TGT GCA CAG GCT GCT GCT GTT GCT GCT GTG   166
Ile Gln Asp Arg Asp Arg Cys Ala Gln Ala Ala Ala Val Ala Ala Val
-50               -45               -40               -35

GGT AAT TTG GAA CCA CGA GGC ACC CCA GGG CCA GAA GAC GAG GCA TTC   214
Gly Asn Leu Glu Pro Arg Gly Thr Pro Gly Pro Glu Asp Glu Ala Phe
              -30               -25               -20

TGT CTG CCT GGA TGT GTG GGA ACT CTC TGC CAA CTT GAT TGG TGG ATC   262
Cys Leu Pro Gly Cys Val Gly Thr Leu Cys Gln Leu Asp Trp Trp Ile
          -15               -10               -5

TGG GGG GGG ATC CAC CCC CAC CCC ACG AGG AAA GCC TGG            301
Trp Gly Gly Ile His Pro His Pro Thr Arg Lys Ala Trp
          1         5               10


(2) INFORMATION FOR SEQ ID NO: 268:
```

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 404 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: CDNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 261..404
            (C) IDENTIFICATION METHOD: fasta
            (D) OTHER INFORMATION: identity 100
                                     region 1..144
                                     id HSU16126
                                     vrt

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 261..353
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 11.3
                                     seq LLLCLLWIGYSQG/TT

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

AGGATTTCTC CCGGATGCTC TCCGACTAAC ATGGATGTCC CACCATTCCT TGCAGTGGAA   60

GGTTGTTCCT TGGCGCAGTG AGTGAAGAAC ATGCAGCGAT TGCTAATGGG TTTGGGAAGC   120

GGAGACTCCT TCCTCTCTCT ATGACCATGC CGTGATCGTG TCTGCGGTCA CCACTCGACG   180

CATCCTCATT TCTACCCGAA CCCAGGAGCC GAACGCTAGA TCGGGGAAGT GGGTGCCGTG   240

CGTGTGGGCA CAGAAACACC ATG AAG ATT ATT TTC CCG ATT CTA AGT AAT CCA   293
                       Met Lys Ile Ile Phe Pro Ile Leu Ser Asn Pro
                       -30   -25

GTC TTC AGG CGC ACC GTT AAA CTC CTG CTC TGT TTA CTG TGG ATT GGA   341
Val Phe Arg Arg Thr Val Lys Leu Leu Leu Cys Leu Leu Trp Ile Gly
-20   -15   -10   -5

TAT TCT CAA GGA ACC ACA CAT GTA TTA AGA TTT GGT GGT ATT TTT GAA   389
Tyr Ser Gln Gly Thr Thr His Val Leu Arg Phe Gly Gly Ile Phe Glu
             1   5   10

TAT GTG GAA TCT GGC   404
Tyr Val Glu Ser Gly
         15

(2) INFORMATION FOR SEQ ID NO: 269:

        (i) SEQUENCE CHARACTERISTICS:

```
         (A) LENGTH: 249 base pairs
         (B) TYPE: NUCLEIC ACID
         (C) STRANDEDNESS: DOUBLE
         (D) TOPOLOGY: LINEAR

  (ii) MOLECULE TYPE: CDNA

  (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

  (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 52..250
         (C) IDENTIFICATION METHOD: fasta
         (D) OTHER INFORMATION:   identity 99
                                  region 2..200
                                  id HS7B2
                                  vrt

  (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 14..250
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 98
                                  region 24..260
                                  id R14271
                                  est

  (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 14..250
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 98
                                  region 25..261
                                  id R18347
                                  est

  (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 14..233
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 97
                                  region 43..262
                                  id H10233
                                  est

  (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 14..240
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 99
                                  region 44..270
                                  id HSCOIE021
                                  est

  (ix) FEATURE:
         (A) NAME/KEY: other
         (B) LOCATION: 42..250
         (C) IDENTIFICATION METHOD: blastn
         (D) OTHER INFORMATION:   identity 98
```

                                            region 1..209
                                            id HSCZSC021
                                            est

          (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: 79..156
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 6.6
                                         seq LFWLASGWTPAFA/YS

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

AAGTTCGCCC GTNTCCTGGC CTGACCCCCA CCAAGGCCCA TACCGCAGTA GGCTCCTCGG   60

GCTGCCCCTC GGTTGACA ATG GTC TCC AGG ATG GTC TCT ACC ATG CTA TCT   111
                    Met Val Ser Arg Met Val Ser Thr Met Leu Ser
                        -25   -20

GGC CTA CTG TTT TGG CTG GCA TCT GGA TGG ACT CCA GCA TTT GCT TAC   159
Gly Leu Leu Phe Trp Leu Ala Ser Gly Trp Thr Pro Ala Phe Ala Tyr
-15   -10   -5   1

AGC CCC CGG ACC CCT GAC CGG GTC TCA GAA GCA GAT ATC CAG AGG CTG   207
Ser Pro Arg Thr Pro Asp Arg Val Ser Glu Ala Asp Ile Gln Arg Leu
                5   10   15

CTT CAT GGT GTT ATG GAG CAA TTG GGC ATT GCC AGG CCC CGG   249
Leu His Gly Val Met Glu Gln Leu Gly Ile Ala Arg Pro Arg
        20   25   30

(2) INFORMATION FOR SEQ ID NO: 270:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 316 base pairs
               (B) TYPE: NUCLEIC ACID
               (C) STRANDEDNESS: DOUBLE
               (D) TOPOLOGY: LINEAR

          (ii) MOLECULE TYPE: CDNA

          (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

          (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 212..311
                (C) IDENTIFICATION METHOD: fasta
                (D) OTHER INFORMATION: identity 93
                                         region 1..101
                                         id HSSCOASN
                                         vrt

          (ix) FEATURE:
                (A) NAME/KEY: other
                (B) LOCATION: 243..311
                (C) IDENTIFICATION METHOD: blastn

```
        (D) OTHER INFORMATION:  identity 94
                                region 60..128
                                id AA135265
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 187..245
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 91
                                region 5..63
                                id AA135265
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 269..311
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 49..91
                                id R58602
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 179..250
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.8
                                seq ATMVSGSSGLAXA/RL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:
```

```
AGAGTTATTA TCTGCSTSTC CGATAGGATG CCTCTTTGTC TTCACCTGCC ATTCCCGCTG    60

TTTCGTGAAG AATCCTCTGT AAAGGGAAAT TTGTTCAGGC GACTGCTGTG GCCACCCTCT   120

GCCTCCTCCG GCCTCTGCCC CTGGGAGGTC CCCGGGGGCC TGGGAGTGTC ATTGGCGT     178

ATG ACC GCA ACC CTT GCC GCT GCC GCT GAC ATC GCT ACC ATG GTC TCC    226
Met Thr Ala Thr Leu Ala Ala Ala Ala Asp Ile Ala Thr Met Val Ser
            -20                 -15                 -10

GGC AGC AGC GGC CTC GCC GNC GCC CGT CTC CTG TCG CGC AST TCC TCC    274
Gly Ser Ser Gly Leu Ala Xaa Ala Arg Leu Leu Ser Arg Xaa Ser Ser
            -5                  1                   5

TGC CGC AGA ATG GAA TTC GGC ATT GTT CCT ACA CAG CCA CGG           316
Cys Arg Arg Met Glu Phe Gly Ile Val Pro Thr Gln Pro Arg
    10                  15                  20
```

```
(2) INFORMATION FOR SEQ ID NO: 271:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN
```

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -14..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 10.8
                                      seq LLLLGLCLGLSLC/VG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val Gly
              -10   -5   1

Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln Asp Gly
        5   10   15

Leu Arg Val Pro Arg
    20

(2) INFORMATION FOR SEQ ID NO: 272:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 79 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -26..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 10.8
                                      seq VLLFFVLLGMSQA/GS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Met Glu Asn Gly Gly Ala Gly Thr Leu Gln Ile Arg Gln Val Leu Leu
    -25   -20   -15

Phe Phe Val Leu Leu Gly Met Ser Gln Ala Gly Ser Glu Thr Gly Asn
-10   -5   1   5

Phe Leu Val Met Glu Glu Leu Gln Ser Gly Ser Phe Val Gly Asn Leu
            10   15   20

Ala Lys Thr Leu Gly Leu Glu Val Ser Glu Leu Ser Ser Arg Gly Ala
        25   30   35

```
Arg Val Val Ser Asn Asp Asn Lys Glu Cys Leu Gln Leu Asp Thr
 40              45              50
```

(2) INFORMATION FOR SEQ ID NO: 273:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 129 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -126..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 10
                                    seq LKLLLFLSTELQA/SQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```
Met Arg Gly Pro Glu Pro Gly Pro Gln Pro Thr Met Glu Gly Asp Val
   -125              -120              -115

Leu Asp Thr Leu Glu Ala Leu Gly Tyr Lys Gly Pro Leu Leu Glu Glu
-110              -105              -100              -95

Gln Ala Leu Thr Lys Ala Ala Glu Gly Gly Leu Ser Ser Pro Glu Phe
              -90              -85              -80

Ser Glu Leu Cys Ile Trp Leu Gly Ser Gln Ile Lys Ser Leu Cys Asn
              -75              -70              -65

Leu Glu Glu Ser Ile Thr Ser Ala Gly Arg Asp Asp Leu Glu Ser Phe
              -60              -55              -50

Gln Leu Glu Ile Ser Gly Phe Leu Lys Glu Met Ala Cys Pro Tyr Ser
   -45              -40              -35

Val Leu Ile Ser Gly Asp Ile Lys Asp Arg Leu Lys Lys Lys Glu Asp
-30              -25              -20              -15

Cys Leu Lys Leu Leu Leu Phe Leu Ser Thr Glu Leu Gln Ala Ser Gln
              -10              -5                        1

Ile
```

(2) INFORMATION FOR SEQ ID NO: 274:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 44 amino acids
            (B) TYPE: AMINO ACID

          .(D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -26..-1
        · (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 9.6
                                  seq WLIALASWSWALC/RI

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
    -25   -20   -15

Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
-10   -5   1   5

Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ser Gly
            10   ·   15

(2) INFORMATION FOR SEQ ID NO: 275:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 89 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -36..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 9.5
                                  seq LGLLLLARHWCIA/GV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Met Gln Gln Thr Arg Thr Glu Ala Val Ala Gly Ala Phe Ser His Cys
    -35   -30   -25

Leu Gly Phe Cys Gly Met Arg Leu Gly Leu Leu Leu Leu Ala Arg His
-20   -15   -10   -5

Trp Cys Ile Ala Gly Val Phe Pro Gln Lys Phe Asp Gly Asp Ser Ala
            1   5   10

Tyr Val Gly Met Ser Asp Gly Asn Pro Glu Leu Leu Ser Thr Ser Gln
        15   20   25

Thr Tyr Asn Gly Gln Ser Glu Asn Asn Glu Asp Tyr Glu Ile Pro Pro
    30   35   40

Ile Thr Pro Pro Asn Leu Pro Glu Ala
45   50

(2) INFORMATION FOR SEQ ID NO: 276:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 53 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -24..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 9.1
                                    seq LVVFLLLPLASGP/QV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met Glu Lys Gly Asn Ala Phe Leu Lys Asn Arg Leu Val Val Phe Leu
            -20   -15   -10

Leu Leu Pro Leu Ala Ser Gly Pro Gln Val Lys Arg Lys Ser Glu Ile
            -5   1   5

Thr Lys Leu Ile Lys Ala Thr Arg Ile Ile Cys Leu Phe Asn Lys Phe
    10   15   20

Ser Arg Gly Asn Gly
25

(2) INFORMATION FOR SEQ ID NO: 277:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 79 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

```
        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -24..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 9
                                       seq LLMLIVFHAASMA/LQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:


Met Phe Pro Phe Asn Gln Ala Gly Leu Pro Thr Leu Leu Met Leu Ile
              -20                 -15                 -10

Val Phe His Ala Ala Ser Met Ala Leu Gln Arg Leu Phe Leu Phe Ala
              -5                  1                   5

Leu Val Trp His Ser Lys Pro Ser Gly Leu Met Thr Gly Lys Leu Glu
    10                  15                  20

Ser Gln Ile Pro His Glu Lys Leu Thr His Ile Ser Val Met His Gly
25                  30                  35                  40

Pro Leu Ser Ser His His Ser Tyr Thr His Ile His Leu Phe Leu
              45                  50                  55



(2) INFORMATION FOR SEQ ID NO: 278:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 99 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -76..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 8.8
                                       seq SLLLWMSSLPSLG/EK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:


Met Thr Ser Arg Ser Leu Arg Arg Cys Ser Cys Leu Arg Val Thr His
    -75                 -70                 -65

Asn Lys Glu Ile Leu Ala Ser Thr Val Ser Leu Gly Val Glu Gly Tyr
-60                 -55                 -50                 -45

Met Leu Gly Gly Gly Ser Arg Ile Asn Ser Ser Asn Leu Asn Asp Gly
              -40                 -35                 -30

Glu Glu Glu Cys Ser Pro Asp Ser Leu Leu Val Trp Lys Lys Lys Ser
              -25                 -20                 -15
```

Leu Leu Leu Trp Met Ser Ser Leu Pro Ser Leu Gly Glu Lys Tyr Phe
        -10   -5   1

Lys Arg Ile Leu Arg Trp Arg Glu His Trp Lys Ser Ser Gly Pro Ile
 5   10   15   20

Pro Leu Trp

(2) INFORMATION FOR SEQ ID NO: 279:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 68 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -53..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.8
                                     seq ILLLLTVLPCIXM/GQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

Met Trp Thr Ala Ser Ala Met Asp Phe Arg Thr Cys Ile Ala Ser Xaa
        -50   -45   -40

Leu Pro Ala Leu Cys Tyr Val Gln Ala Cys Arg Ala Leu Met Ile Ala
        -35   -30   -25

Ala Ser Val Leu Gly Leu Pro Ala Ile Leu Leu Leu Leu Thr Val Leu
        -20   -15   -10

Pro Cys Ile Xaa Met Gly Gln Glu Pro Gly Val Ala Lys Tyr Arg Xaa
 -5   1   5   10

Ala Gln Leu Ala
            15

(2) INFORMATION FOR SEQ ID NO: 280:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 86 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:

. (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: -45..-1
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 8.5
                            seq FALLSLSHPTCQA/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Met Gly Pro Pro Pro Thr His Ile Lys Tyr Leu His Leu Asn Ile Tyr
-45   -40   -35   -30

Cys Asn Gly Lys Ser Thr Ala Pro Gly Ile Arg Ser His Ser Leu Gly
            -25   -20   -15

Phe Ala Leu Leu Ser Leu Ser His Pro Thr Cys Gln Ala Gly Ala Pro
            -10   -5   1

Ala Ala Ala Leu Pro Ser Leu Trp Ser Trp Cys Ser Arg Gly Ala Arg
    5   10   15

Val Arg Val Gly Arg Met Leu Ser His Leu Tyr Thr Cys Gly Trp Tyr
20   25   30   35

Asp His Asn Pro His Gly
            40

(2) INFORMATION FOR SEQ ID NO: 281:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -16..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.5
                                seq LLTFLAFTTLLFA/PP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Met Phe Cys Leu Leu Thr Phe Leu Ala Phe Thr Thr Leu Leu Phe Ala
    -15   -10   -5

Pro Pro Trp
    1

(2) INFORMATION FOR SEQ ID NO: 282:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 80 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -29..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.4
                        seq LKCLLAVLSSLFA/AI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

Met His Cys Gly Ser Thr Pro Gly Leu Cys Pro Cys Trp Val Pro Phe
         -25   -20   -15

Leu Lys Cys Leu Leu Ala Val Leu Ser Ser Leu Phe Ala Ala Ile Ser
         -10   -5   1

Val Asp Arg Leu Tyr Leu Ser Phe Cys Ser Asn Cys Ser Glu Ile Tyr
  5   10   15

Leu Trp Pro Pro Ser Phe Pro Ala Pro Pro Ser Pro Val Val Leu Leu
20   25   30   35

Val Phe Leu Cys Pro His Gly Thr Ser Leu Ser Phe Leu Lys Leu Pro
         40   45   50

(2) INFORMATION FOR SEQ ID NO: 283:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -16..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.3

seq VCSALLLLGIVSS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

Met Asn Leu Val Cys Ser Ala Leu Leu Leu Leu Gly Ile Val Ser Ser
    -15   -10   -5

Lys Pro Tyr Met Arg Lys Arg
  1   5

(2) INFORMATION FOR SEQ ID NO: 284:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 47 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -35..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.3
                              seq AAMLIGLLAWLQT/VP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

Met Ser Val Leu Asp Asp Arg Gln Arg Asp Ile Leu Val Val Gln Lys
-35   -30   -25   -20

Arg His Ser Ser Leu Glu Ala Ala Met Leu Ile Gly Leu Leu Ala Trp
              -15   -10   -5

Leu Gln Thr Val Pro Ala His Gly Cys Gln Phe Leu Pro Ile Arg
              1   5   10

(2) INFORMATION FOR SEQ ID NO: 285:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 38 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:

```
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -20..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 8.3
                                      seq LLIICHYLPLSLC/IP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:


Met Gly Val Asn Gly Arg Arg Leu Leu Ile Ile Cys His Tyr Leu Pro
-20               -15               -10                       -5

Leu Ser Leu Cys Ile Pro Ile Pro Ser His Ile Asn Ser Leu Pro Arg
                 1           5               10

Asn Thr Pro Pro Val Arg
          15




  (2) INFORMATION FOR SEQ ID NO: 286:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 43 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

       (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -31..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 8.2
                                      seq LECLLLYLAESSG/LR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:


Met Lys Leu Arg Glu Cys Pro Ala Leu Arg Trp Ser Gln Leu Ser Gln
    -30               -25               -20

His Lys Leu Glu Cys Leu Leu Leu Tyr Leu Ala Glu Ser Ser Gly Leu
-15               -10                     -5                     1

Arg Thr Gly Asn Val Gly Val Leu His Pro Arg
             5               10




  (2) INFORMATION FOR SEQ ID NO: 287:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 136 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR
```

```
(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Homo Sapiens
     (F) TISSUE TYPE: Brain

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: -109..-1
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:   score 8.2
                              seq LLRLPQLPPXCSA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:


Met Asp Pro Arg Gly Ile Leu Lys Ala Phe Pro Lys Arg Gln Lys Ile
              -105                -100                -95

His Ala Asp Ala Ser Ser Lys Val Leu Ala Lys Ile Pro Arg Arg Glu
              -90              -85              -80

Glu Gly Glu Glu Ala Glu Glu Trp Leu Ser Ser Leu Arg Ala His Val
          -75              -70              -65

Val Arg Thr Gly Ile Gly Arg Ala Arg Ala Glu Leu Phe Glu Lys Gln
    -60              -55              -50

Ile Val Gln His Gly Gly Gln Leu Cys Pro Ala Gln Gly Pro Gly Val
-45              -40              -35                        -30

Thr His Ile Val Val Asp Glu Gly Met Asp Tyr Glu Arg Ala Leu Arg
              -25              -20                        -15

Leu Leu Arg Leu Pro Gln Leu Pro Pro Xaa Cys Ser Ala Gly Glu Val
              -10              -5                         1

Ser Leu Ala Glu Leu Val Pro Ser Gly Glu Glu Ala Gly Gly Cys Ser
    5                10               15

Trp Ile Gln His Leu His Pro Ser
20                  25
```

```
(2) INFORMATION FOR SEQ ID NO: 288:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -21..-1
```

```
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 8
                                      seq LFLVAVLVKVAEA/RK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:


Met Phe Trp Lys Leu Ser Leu Ser Leu Phe Leu Val Ala Val Leu Val
    -20               -15               -10

Lys Val Ala Glu Ala Arg Lys Asn Arg Ser
    -5                1                5




(2) INFORMATION FOR SEQ ID NO: 289:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 26 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -18..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 7.9
                                      seq LFSLLVLQSMATG/AT

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:


Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala
        -15               -10                        -5

Thr Gly Ala Thr Phe Pro Glu Glu Ala Pro
        1                5




(2) INFORMATION FOR SEQ ID NO: 290:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 70 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
```

          (B) LOCATION: -18..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 7.9
                                 seq LFSLLVLQSMATG/AT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala
         -15   -10   -5

Thr Gly Ala Thr Phe Pro Glu Glu Ala Ile Ala Asp Leu Ser Val Asn
         1   5   10

Met Tyr Asn Arg Leu Arg Ala Val Gly Ser Trp Arg Arg Glu Gly Ala
 15   20   25   30

Ser Arg Gln Ile Ala Ser Cys Leu Pro Ala Phe Leu Leu His Leu Pro
             35   40   45

Leu Thr His Thr His Gly
             50

(2) INFORMATION FOR SEQ ID NO: 291:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 103 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -55..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.8
                                   seq ALLVALLFTLIHR/RR

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Met Ser Phe Ser Leu Asn Phe Thr Leu Pro Ala Asn Thr Thr Ser Ser
-55   -50   -45   -40

Pro Val Thr Gly Gly Lys Glu Thr Asp Cys Gly Pro Ser Leu Gly Leu
             -35   -30   -25

Ala Ala Gly Ile Pro Leu Leu Val Ala Thr Ala Leu Leu Val Ala Leu
             -20   -15   -10

Leu Phe Thr Leu Ile His Arg Arg Arg Ser Ser Ile Glu Ala Met Glu
         -5   1   5

Glu Ser Asp Arg Pro Cys Glu Ile Ser Glu Ile Asp Asp Asn Pro Lys

```
          10                 15                 20                 25

Ile Ser Glu Asn Pro Arg Arg Ser Pro Thr His Glu Lys Asn Thr Met
                    30                 35                 40

Gly Ala Gln Glu Ala Arg Trp
                45
```

(2) INFORMATION FOR SEQ ID NO: 292:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 82 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -80..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 7.7
                            seq LVLFLSLALLVTP/TS

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```
Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
-80              -75              -70                           -65

Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
                -60              -55                  -50

Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
                -45              -40                  -35

Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser
        -30              -25                  -20

Val Asp Pro Leu Val Leu Phe Leu Ser Leu Ala Leu Leu Val Thr Pro
    -15              -10                  -5

Thr Ser
  1
```

(2) INFORMATION FOR SEQ ID NO: 293:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 43 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

```
        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -19..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 7.7
                                     seq LQLLCCIFTLVLQ/HY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:
```

```
Met Ala Ile Gly Ile Ser Leu Gln Leu Leu Cys Cys Ile Phe Thr Leu
            -15               -10                     -5

Val Leu Gln His Tyr Leu Leu Gly Ser His Pro Tyr Ile Thr Cys Ile
             1               5                   10

His Ser Gln Leu Leu Leu Asp Ile Gln Gln Gln
    15                  20
```

```
(2) INFORMATION FOR SEQ ID NO: 294:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 74 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -19..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 7.6
                                     seq LLNLLLLSLFAGL/DP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:
```

```
Met Gln Ala Thr Ser Asn Leu Leu Asn Leu Leu Leu Leu Ser Leu Phe
            -15               -10                     -5

Ala Gly Leu Asp Pro Ser Lys Asn Lys Lys Arg Gly Ser Ser Phe Ser
             1               5                   10

Phe Lys Phe Pro Leu Leu Asp Asp Thr Pro Phe Leu Xaa Ser Arg Ile
    15                  20                  25

Glu Asn Ser Ala Thr His His Leu His Tyr Gly Leu Asn Met Ile Leu
    30                  35                  40                  45
```

Trp Val Asn Trp Lys Pro Lys Leu Thr Leu
          50   55

(2) INFORMATION FOR SEQ ID NO: 295:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 34 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -31..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 7.6
                                     seq VTLLCGWPGSHWC/AP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Met Lys Trp Lys Pro Glu Asp Leu Gly Ser Val Pro Cys Glu Ala
     -30   -25   -20

Phe Ser Val Thr Leu Leu Cys Gly Trp Pro Gly Ser His Trp Cys Ala
 -15   -10   -5   1

Pro Pro

(2) INFORMATION FOR SEQ ID NO: 296:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 78 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -19..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 7.6
                                     seq LLNLLLLSLFAGL/DP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```
Met Gln Ala Thr Ser Asn Leu Leu Asn Leu Leu Leu Leu Ser Leu Phe
            -15             -10                       -5

Ala Gly Leu Asp Pro Ser Lys Thr Gln Ile Ser Pro Lys Glu Gly Trp
             1               5               10

Gln Val Tyr Ser Ser Ala Gln Asp Pro Asp Gly Arg Cys Ile Cys Thr
        15              20              25

Val Val Ala Pro Glu Gln Asn Leu Cys Ser Arg Asp Ala Lys Ser Arg
   30              35              40                       45

Gln Leu Arg Gln Leu Leu Glu Lys Val Gln Asn Met Ser Arg
            50              55
```

(2) INFORMATION FOR SEQ ID NO: 297:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 80 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -48..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.5
                                  seq FVILLLFIFTVVS/LV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```
Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
            -45             -40                   -35

Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
        -30             -25                   -20

Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
        -15             -10                   -5

Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
    1               5               10                  15

Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Arg
            20              25                  30
```

(2) INFORMATION FOR SEQ ID NO: 298:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 35 amino acids

```
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -33..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 7.4
                                seq ITCCVLLLLNCSG/VW

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:
```

```
Met Leu Trp Phe Ser Gly Val Gly Ala Leu Ala Glu Arg Tyr Cys Arg
        -30                 -25                 -20

Arg Ser Pro Gly Ile Thr Cys Cys Val Leu Leu Leu Leu Asn Cys Ser
        -15                 -10                 -5

Gly Val Trp
        1
```

```
(2) INFORMATION FOR SEQ ID NO: 299:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -25..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 7.3
                                    seq LIFFLNVTQLVRG/RG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:
```

```
Met Leu Phe Leu Gln Met Gly Lys Gln Ser Trp Thr Leu Ile Phe Phe
-25                 -20                 -15                 -10

Leu Asn Val Thr Gln Leu Val Arg Gly Arg Gly Pro Gly Gly Arg
            -5                  1                   5
```

(2) INFORMATION FOR SEQ ID NO: 300:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -27..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.2
                                    seq LLLGLCSPPXXSL/AS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Glu Leu Arg Xaa Xaa Pro Pro Gly Gly Arg Glu Val Gln Leu Leu
     -25   -20   -15

Leu Gly Leu Cys Ser Pro Pro Xaa Xaa Ser Leu Ala Ser Phe Pro Lys
     -10   -5   1   5

Ala Ala Gln Met

(2) INFORMATION FOR SEQ ID NO: 301:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -14..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7
                                    seq LWSLLSSSGSHFG/IP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Leu Trp Ser Leu Leu Ser Ser Ser Gly Ser His Phe Gly Ile Pro
             -10   -5   1

His His Thr Phe Pro Gln Glu Gly
     5   10

(2) INFORMATION FOR SEQ ID NO: 302:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 112 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -52..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7
                            seq SVWLCLLCYFAFP/FQ

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Met Asp Ile Ser Gly Leu Ile Pro Gly Leu Val Ser Thr Phe Ile Leu
      -50   -45   -40

Leu Ser Xaa Ser Asp His Tyr Gly Arg Lys Phe Pro Met Ile Leu Ser
    -35   -30   -25

Ser Val Gly Ala Leu Ala Thr Ser Val Trp Leu Cys Leu Leu Cys Tyr
-20   -15   -10   -5

Phe Ala Phe Pro Phe Gln Leu Leu Ile Ala Ser Thr Phe Ile Gly Ala
         1   5   10

Phe Xaa Gly Asn Tyr Thr Thr Phe Trp Gly Ala Cys Phe Ala Tyr Ile
    15   20   25

Val Asp Gln Cys Lys Glu Xaa Xaa Gln Lys Thr Ile Arg Ile Ala Ile
    30   35   40

Ile Asp Phe Leu Leu Gly Leu Val Thr Gly Leu Thr Val Leu Ser Ser
 45   50   55   60

(2) INFORMATION FOR SEQ ID NO: 303:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -30..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 7
                                    seq LFVILLITSLIFC/SL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:


Met Xaa Val Phe Phe Ser Lys Asn Arg Phe Glu Met Tyr Phe Ser Leu
-30                 -25             -20                     -15

Leu Leu Phe Val Ile Leu Leu Ile Thr Ser Leu Ile Phe Cys Ser Leu
            -10                 -5                      1

Tyr Val Ala Arg
        5
```

(2) INFORMATION FOR SEQ ID NO: 304:

```
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 34 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -23..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION:  score 6.9
                                    seq SLSLLASHHSVSC/SN

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:


Met Pro Val Pro Ala Cys Trp Ile Ser Ser Ser Leu Ser Leu Leu Ala
        -20             -15             -10

Ser His His Ser Val Ser Cys Ser Asn Ile Phe Leu Asn Phe Asn Pro
        -5              1               5

Asp Arg
10
```

(2) INFORMATION FOR SEQ ID NO: 305:

```
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 59 amino acids
              (B) TYPE: AMINO ACID
```

        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -21..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.9
                                seq LLACGSLLPGLWQ/HL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala Cys Gly Ser Leu Leu
    -20   -15   -10

Pro Gly Leu Trp Gln His Leu Thr Ala Asn His Trp Pro Pro Phe Ser
    -5   1   5   10

Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser Glu Gln Ile Ser Glu
        15   20   25

Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Leu
        30   35

(2) INFORMATION FOR SEQ ID NO: 306:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -76..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.9
                                seq LLPLSAWPPWAWH/HH

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Met Ala Leu Thr Ile His Gly Glu Arg Met Arg Pro Asp Trp Glu Ser
    -75   -70   -65

Pro Trp Ile Thr Ser Ser Gln Ala Gln Ser Leu Ser Leu Gly Gly Ser
    -60   -55   -50   -45

```
Pro Ser Ser Arg Gly Pro Leu Val Pro Arg Gly Glu Tyr Leu Ala Ser
            -40                -35                -30

Cys Pro Glu Gly Val Arg Ser His Ser His Leu Leu Pro Arg Ser Leu
            -25                -20                -15

Leu Pro Leu Ser Ala Trp Pro Pro Trp Ala Trp His His His Gly Pro
            -10                -5                  1

Gly Thr Gln Ser Leu Val Gly Cys Leu Cys Ala Met Ser Pro Leu Leu
  5                10                15                20

Pro Thr His Leu Ser Leu Pro Val Leu Glu Pro Ser Gly Thr Pro Ala
            25                30                35

Leu Lys Asp Arg Arg Pro Cys Glu Val Gly Ile Pro Ile Pro Pro Arg
            40                45                50
```

(2) INFORMATION FOR SEQ ID NO: 307:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 95 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -92..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.8
                                  seq ILIASSLPTLSHP/AP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```
Met Ala Ala Arg Phe Arg Cys Gly His Leu Cys Val Pro Glu Val Pro
        -90                -85                -80

Arg Gly Pro Ala Ser His Ala Glu Gly Gly Gly Gly Arg Leu Ser Arg
    -75                -70                -65

Lys Ala Ala His Gln Ala Gln Leu Cys Trp Arg Ala Gly Gly Asp Gly
-60                -55                -50                -45

Arg Gly Asn Phe Asn Pro Met Asn Phe Leu Val Ala Gly Thr Phe Ala
            -40                -35                -30

Ser Ser Cys His Ser Pro Pro Leu Leu Trp Ser Leu Pro Pro Arg Ile
            -25                -20                -15

Leu Ile Ala Ser Ser Leu Pro Thr Leu Ser His Pro Ala Pro Gly
        -10                -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 308:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 87 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -29..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.8
                                  seq VLSLICSCFYTQP/HP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Ala Ser Thr Ile Ser Ala Tyr Lys Glu Lys Met Lys Glu Leu Ser
         -25   -20   -15

Val Leu Ser Leu Ile Cys Ser Cys Phe Tyr Thr Gln Pro His Pro Asn
         -10   -5   1

Thr Val Tyr Gln Tyr Gly Asp Met Glu Val Lys Gln Leu Asp Lys Arg
   5   10   15

Ala Ser Gly Gln Ser Phe Glu Val Ile Leu Lys Ser Pro Ser Asp Leu
20   25   30   35

Ser Pro Glu Ser Pro Met Leu Ser Ser Pro Pro Lys Lys Lys Asp Thr
         40   45   50

Ser Leu Glu Glu Leu Gln Lys
        55

(2) INFORMATION FOR SEQ ID NO: 309:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 120 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -114..-1

```
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 6.7
                                seq LIPMAILLGQTQS/NS

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:
```

Met Leu Gln Val Tyr Gly Lys Pro Val Tyr Gln Gly His Arg Ser Thr
          -110   -105   -100

Leu Lys Lys Gly Pro Tyr Leu Arg Phe Asn Ser Pro Ser Pro Lys Ser
          -95   -90   -85

Arg Pro Gln Arg Pro Lys Val Ile Glu Arg Val Lys Gly Thr Lys Val
         -80   -75   -70

Lys Ser Ile Arg Thr Gln Thr Asp Phe Tyr Ala Thr Lys Pro Lys Lys
         -65   -60   -55

Met Asp Ser Lys Met Lys His Ser Val Pro Val Leu Pro His Gly Asp
-50   -45   -40   -35

Gln Gln Tyr Leu Phe Ser Pro Ser Arg Glu Met Pro Thr Phe Ser Gly
          -30   -25   -20

Thr Leu Glu Gly His Leu Ile Pro Met Ala Ile Leu Leu Gly Gln Thr
          -15   -10   -5

Gln Ser Asn Ser Asp Thr Met Pro
     1   5

(2) INFORMATION FOR SEQ ID NO: 310:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 127 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -118..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.7
                                seq LLFAKLFGHLTSA/RR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:
```

Met Ser Val Leu Glu Ile Ser Gly Met Ile Met Asn Arg Val Asn Ser
        -115              -110             -105

His Ile Pro Gly Ile Gly Tyr Gln Ile Phe Gly Asn Ala Val Ser Leu
        -100              -95              -90

```
Ile Leu Gly Leu Thr Pro Phe Val Phe Arg Leu Ser Gln Ala Thr Asp
    -85             -80             -75
```

```
Leu Glu Gln Leu Thr Ala His Ser Ala Ser Glu Leu Tyr Val Ile Ala
-70             -65             -60                     -55
```

```
Phe Gly Ser Asn Glu Asp Val Ile Val Leu Ser Met Val Ile Ile Ser
            -50             -45                     -40
```

```
Phe Val Val Arg Val Ser Leu Val Trp Ile Phe Phe Phe Leu Leu Cys
        -35             -30                 -25
```

```
Val Ala Glu Arg Thr Tyr Lys Gln Arg Leu Leu Phe Ala Lys Leu Phe
    -20             -15                 -10
```

```
Gly His Leu Thr Ser Ala Arg Arg Ala Arg Lys Ser Glu Val Pro
    -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 311:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 71 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -69..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6.7
                           seq FFKLLLLGAMCSG/AR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```
Met Cys Lys Gly Ile Lys Ala Gly Asp Thr Cys Glu Lys Leu Val Gly
            -65             -60             -55
```

```
Tyr Ser Ala Val Tyr Arg Val Cys Phe Gly Met Ala Cys Phe Phe Phe
        -50             -45                 -40
```

```
Ile Phe Cys Leu Leu Thr Leu Lys Ile Asn Asn Ser Lys Ser Cys Arg
        -35             -30                 -25
```

```
Ala His Ile His Asn Gly Phe Trp Phe Phe Lys Leu Leu Leu Leu Gly
    -20             -15             -10
```

```
Ala Met Cys Ser Gly Ala Arg
 -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 312:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 114 amino acids
       (B) TYPE: AMINO ACID
       (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Homo Sapiens
       (F) TISSUE TYPE: Brain

    (ix) FEATURE:
       (A) NAME/KEY: sig_peptide
       (B) LOCATION: -104..-1
       (C) IDENTIFICATION METHOD: Von Heijne matrix
       (D) OTHER INFORMATION: score 6.6
                          seq HFSHVVWFHPTWA/QQ

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Ser Asp Ser Ala Gly Gly Arg Ala Gly Leu Arg Arg Tyr Pro Lys
          -100   -95   -90

Leu Pro Val Trp Val Val Glu Asp His Gln Glu Val Leu Pro Phe Ile
        -85   -80   -75

Tyr Arg Ala Ile Gly Ser Lys His Leu Pro Ala Ser Asn Val Ser Phe
    -70   -65   -60

Leu His Phe Asp Ser His Pro Asp Leu Leu Ile Pro Val Asn Met Pro
  -55   -50   -45

Ala Asp Thr Val Phe Asp Lys Glu Thr Leu Phe Gly Glu Leu Ser Ile
-40   -35   -30   -25

Glu Asn Trp Ile Met Pro Ala Val Tyr Ala Gly His Phe Ser His Val
        -20   -15   -10

Val Trp Phe His Pro Thr Trp Ala Gln Gln Ile Arg Glu Gly Arg His
       -5   1   5

His Phe
  10

(2) INFORMATION FOR SEQ ID NO: 313:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 109 amino acids
       (B) TYPE: AMINO ACID
       (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Homo Sapiens
       (F) TISSUE TYPE: Brain

```
        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -47..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 6.3
                                seq SSCVLLTALVALA/AY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:


Met Ser Ser Cys Arg Gly Gln Lys Val Ala Gly Gly Leu Arg Val Val
        -45                 -40                 -35

Ser Pro Phe Pro Leu Cys Gln Pro Ala Gly Glu Pro Ser Arg Gly Lys
        -30                 -25                 -20

Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala Leu Ala Ala
-15                 -10                 -5                       1

Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp Pro Trp Lys
                5                 10                  15

Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Xaa Xaa Xaa Ser Xaa
        20                  25                  30

Leu Val Xaa Tyr Leu Gly Leu Ser Xaa His Leu Leu Ala Leu Xaa Xaa
    35                  40                  45

Xaa Leu Phe Leu Leu Ala Lys Lys Ala Arg Gly Leu Leu
50                  55                  60



(2) INFORMATION FOR SEQ ID NO: 314:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 72 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -42..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 6.1
                                seq DLAVALSLLPAWT/ES

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:


Met Ile Ile Pro Phe Lys Ile Lys Asn Leu Gly Gly Arg Val Leu Leu
        -40                 -35                 -30

Ser Gly Arg Glu Met Phe Pro Ala Ser Val Arg Ala Pro Asp Leu Ala
```

```
        -25                 -20                 -15

Val Ala Leu Ser Leu Leu Pro Ala Trp Thr Glu Ser Pro Thr Arg Gly
-10                 -5                  1                   5

Ser His Gln Ser Gln Ala Arg Ala His Ser Arg Ala Leu Arg Lys Gln
            10                  15                  20

Ser Arg Asn Thr Arg Ser Pro Arg
            25                  30
```

(2) INFORMATION FOR SEQ ID NO: 315:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -53..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6
                            seq ALILLLLAQKGPS/XF

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```
Met Val Cys Ser Ala Pro Arg Lys Ile Val Val Arg Ala Phe Ile Thr
        -50                 -45                 -40

Ile Ile Phe Ile Tyr Tyr Ala Ile Lys Lys Arg Ala Asn Glu Pro Ala
    -35                 -30                 -25

Ala Tyr Leu Met Leu Lys Pro Glu Ala Leu Ile Leu Leu Leu Leu Ala
    -20                 -15                 -10

Gln Lys Gly Pro Ser Xaa Phe Leu Leu Val Trp Arg
-5                  1                   5
```

(2) INFORMATION FOR SEQ ID NO: 316:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

         (F) TISSUE TYPE: Brain

   (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: -40..-1
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 5.9
                                 seq VCSALCSLGEVRP/XE

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Thr Glu Ser Ser Met Lys Lys Leu Ala Ser Thr Leu Leu Asp Ala
-40   -35   -30   Thr   -25

Ile Thr Asp Lys Asp Pro Leu Val Gln Glu Gln Val Cys Ser Ala Leu
         -20   -15   -10

Cys Ser Leu Gly Glu Val Arg Pro Xaa Glu Thr Leu Arg Ala Cys Glu
         -5   1   5

Glu Tyr Leu Arg Xaa Met Thr Ser Trp His Thr Arg
    10   15   20

(2) INFORMATION FOR SEQ ID NO: 317:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 59 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -43..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 5.9
                                  seq VFLFHCTSGLSSC/KC

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Gln Glu Thr Asp Cys Asn Lys Arg Trp Gly Arg Gly Leu Gly Gly
         -40   -35   -30

Leu Trp Ser Glu Thr Gly Arg Arg Phe His Cys Lys Ser Phe Val Phe
    -25   -20   -15

Leu Phe His Cys Thr Ser Gly Leu Ser Ser Cys Lys Cys Ser Lys Lys
    -10   -5   1   5

His Xaa Lys Tyr Cys Phe Cys Phe Val Ala Ser
        10   15

```
Ser Pro Ala Phe Leu Ala Val Ala Gly Pro Gly Trp Ala Arg Pro Gly
         -10                  -5                   1

Cys Xaa Leu Arg Thr Lys Tyr Asp Ser Gln Leu Ala Arg His Leu Leu
     5               10                  15

Gln Pro Gln Phe Pro Gly Leu Thr Leu Gly Thr Leu Val Gln Pro Ala
 20              25                  30                      35

His Trp Gly Met Gly Gly Gly Thr Gly Gly Val Leu Gly Glu Gly Gly
             40                  45                      50

Gly His Ser Tyr Ala Glu His Gly Thr Cys Leu Gln Ser Cys Ser Thr
             55                  60                  65

Asp Val Leu Xaa His Val Leu Leu Ala
         70                  75
```


(2) INFORMATION FOR SEQ ID NO: 320:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 125 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -18..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.6
                                    seq WHFLASFFPRAGC/HG

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```
Met Leu Gln Met Leu Trp His Phe Leu Ala Ser Phe Phe Pro Arg Ala
         -15                 -10                  -5

Gly Cys His Gly Ser Arg Glu Gly Asp Asp Arg Glu Val Arg Gly Thr
         1               5                   10

Pro Ala Pro Ala Trp Arg Asp Gln Met Ala Ser Phe Leu Gly Lys Gln
 15              20                  25                      30

Asp Gly Arg Ala Glu Ala Thr Glu Lys Arg Pro Thr Ile Leu Leu Val
             35                  40                      45

Val Gly Pro Ala Glu Gln Phe Pro Lys Lys Ile Val Gln Ala Gly Asp
         50                  55                  60

Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu
     65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO: 318:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -17..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.8
                                seq VPWLSSTVSCAQG/LR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Leu Leu Glu Val Pro Trp Leu Ser Ser Thr Val Ser Cys Ala Gln
        -15   -10   -5

Gly Leu Arg Leu Ala Gln His Arg Val Pro Phe Phe Tyr Ser Asn Val
    1   5   10   15

Ser Leu Cys Lys Leu Leu Leu Pro Ala Xaa Leu His Gly
            20   25

(2) INFORMATION FOR SEQ ID NO: 319:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 105 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -29..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.7
                                seq SPAFLAVAGPGWA/RP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Ser Gly Gly Arg Met Gln Ala Arg Cys Ser Gln Gln Ser Thr Trp
        -25   -20   -15

Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys
    80   85   90

Lys Asn Asp Gly Arg Ile Asp Ala Gln Glu Ile Met Gln
95   100   105

(2) INFORMATION FOR SEQ ID NO: 321:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 37 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: -20..-1
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 5.6
                                    seq SLVCLLAMGKGLG/SS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Tyr Ser His Pro Val Ser Ser Leu Val Cys Leu Leu Ala Met Gly
-20   -15   -10   -5

Lys Gly Leu Gly Ser Ser Gln Ala Leu Val Gln Pro Asp Thr Trp Pro
                 1   5   10

His Thr Ser Pro Arg
         15

(2) INFORMATION FOR SEQ ID NO: 322:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 92 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: -35..-1
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 5.6

seq FIFMEVLGSGAFS/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```
Met Gly Arg Lys Glu Glu Asp Asp Cys Ser Xaa Trp Lys Lys Gln Thr
-35               -30           -25            Trp         -20

Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly Ser Gly
            -15             -10                      -5

Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly Lys Leu
            1           5               10

Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp Ser Ser
    15              20              25

Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu Asn Ile
    30              35              40                      45

Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Gln Gly
            50                      55
```

(2) INFORMATION FOR SEQ ID NO: 323:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 48 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -29..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.6
                                   seq LLPNQSLFSLARA/VR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

```
Met Met Ile Ala Val Phe Gly Asn Ala Asn Asp Arg Asn Val Leu Thr
            -25             -20              -15

Leu Leu Pro Asn Gln Ser Leu Phe Ser Leu Ala Arg Ala Val Arg Asn
            -10             -5               1

His Leu Leu Leu Glu Glu Arg Arg Leu Thr Thr Tyr Gly Val Leu Cys
    5               10              15
```

(2) INFORMATION FOR SEQ ID NO: 324:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -19..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.6
                                seq LVVTAWFFGMCRS/KA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Phe Phe Glu Leu Pro Leu Val Val Thr Ala Trp Phe Phe Gly Met
            -15   -10   -5

Cys Arg Ser Lys Ala Leu Leu Gly Asn Ala Arg Ser Ala Leu Cys Leu
            1   5   10

Gln Thr Lys Ala Cys Ala Ser Ser Thr Gln Pro Asp Thr His Asn Glu
    15   20   25

His His Pro Arg Asn Pro Cys Pro Tyr Leu
30   35

(2) INFORMATION FOR SEQ ID NO: 325:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 54 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -44..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.5
                                seq FLLIVANVHFSQT/WV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Asn His Asn Ile Ile Ile Cys Val Met Tyr Ile Val Pro Phe Leu
            -40   -35   -30

```
Met Thr Lys Cys Leu Tyr Phe Cys His Ser Cys Lys Arg Gly Ser Phe
          -25                 -20             -15

Leu Leu Ile Val Ala Asn Val His Phe Ser Gln Thr Trp Val Phe Ser
          -10                 -5                  1

Gly Lys Pro Tyr Lys Gly
  5               10
```

(2) INFORMATION FOR SEQ ID NO: 326:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 53 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -21..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.5
                          seq LTGLCXCCLQALG/LA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```
Met Ser Cys Gly Ser Ala Ala Ser Leu Thr Gly Leu Cys Xaa Cys Cys
      -20             -15                 -10

Leu Gln Ala Leu Gly Leu Ala Trp Arg Arg Arg Gly Leu Thr Gly Pro
  -5                  1               5                  10

Gly Leu Pro Pro Val Leu Gln Ile Cys Cys Pro Arg Ser Leu Arg Gly
              15                 20              25

Val Thr Ala Pro Thr
          30
```

(2) INFORMATION FOR SEQ ID NO: 327:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -46..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 5.4
                                     seq VLFFVGLITNGLA/MR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:


Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
   -45             -40             -35

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
-30             -25             -20                         -15

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
                -10             -5                          1

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
        5               10              15

Asn Thr Val Lys
   20




(2) INFORMATION FOR SEQ ID NO: 328:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 28 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -20..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION:  score 5.3
                                     seq LCSSCCSWGPAAG/AL

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:


Met Ala Ala Ala Met Xaa Leu Leu Cys Ser Ser Cys Cys Ser Trp Gly
-20             -15             -10                         -5

Pro Ala Ala Gly Ala Leu Gln Asn Pro Gln Arg Gly
                1               5




(2) INFORMATION FOR SEQ ID NO: 329:

        (i) SEQUENCE CHARACTERISTICS:
```

           (A) LENGTH: 30 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

       (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -25..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION: score 5.3
                                     seq SVVKVLSLRKAQA/QS

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Asp Phe Ile Lys Asp Gln Ser Leu Ser His Arg Ser Val Val Lys
-25   -20   -15   -10

Val Leu Ser Leu Arg Lys Ala Gln Ala Gln Ser Ile Leu Glu
            -5   1   5

(2) INFORMATION FOR SEQ ID NO: 330:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 75 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

       (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -28..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION: score 5.3
                                     seq RISCAFSLASSTA/RQ

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Thr Arg Pro Phe Trp Ala Ser Cys Ser Thr Trp Ala Thr Ser Arg
            -25   -20   -15

Ile Ser Cys Ala Phe Ser Leu Ala Ser Ser Thr Ala Arg Gln Thr Ser
            -10   -5   1

Ile Ala Cys Cys Ala Thr His Arg Thr Ala Trp Ala Ser Arg Pro Gly
  5   10   15   20

Pro Arg Arg Pro Trp Cys Cys Arg Tyr Ser Lys Pro Leu Thr Thr Trp

                25   30   35

Pro Val Arg Met Met Arg Arg Glu Gly Ser Xaa
             40   45

(2) INFORMATION FOR SEQ ID NO: 331:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 35 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -16..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 5.3
                              seq CAVSLTTAAVAFG/DE

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Lys Ser Cys Ala Val Ser Leu Thr Thr Ala Ala Val Ala Phe Gly
    -15   -10   -5

Asp Glu Ala Lys Lys Met Ala Glu Gly Lys Ala Ser Arg Glu Ser Glu
 1   5   10   15

Glu Glu Thr

(2) INFORMATION FOR SEQ ID NO: 332:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 39 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -21..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 5.2
                              seq LSLSLICLRMSLS/LY

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

```
Met Ser Ile His Glu Cys Ala Cys Leu Ser Leu Ser Leu Ile Cys Leu
    -20             -15             -10
```

```
Arg Met Ser Leu Ser Leu Tyr Pro Pro Pro Ala Ser Met Ile Leu Leu
 -5                  1             5                      10
```

```
Pro Gln Thr Trp Lys Pro Arg
             15
```

(2) INFORMATION FOR SEQ ID NO: 333:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 42 amino acids
       (B) TYPE: AMINO ACID
       (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Homo Sapiens
       (F) TISSUE TYPE: Brain

    (ix) FEATURE:
       (A) NAME/KEY: sig_peptide
       (B) LOCATION: -15..-1
       (C) IDENTIFICATION METHOD: Von Heijne matrix
       (D) OTHER INFORMATION: score 5.2
                       seq SGLSFLSVFSLWC/EP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

```
Met Leu Ser Gly Leu Ser Phe Leu Ser Val Phe Ser Leu Trp Cys Glu
-15             -10             -5                          1
```

```
Pro Thr Leu Pro Ala Leu Gly Asn Gly Ser Val Leu Gly Val Arg Xaa
             5                  10                      15
```

```
Ser Ser Ser Ser Ser Ala Gln Cys Ser Leu
         20                  25
```

(2) INFORMATION FOR SEQ ID NO: 334:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 87 amino acids
       (B) TYPE: AMINO ACID
       (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Homo Sapiens
       (F) TISSUE TYPE: Brain

    (ix) FEATURE:

        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -85..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.2
                                seq LYSILHFPFWVHG/RX

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Gly Leu Lys Asp Lys Ser Gln Ala Pro Ala Ser Gly Leu Gly Val
-85   -80   -75   -70

Leu Arg Gly Gln Arg Ser Gly Ser Phe Ile Ser Met Pro Ala Pro Ala
            -65   -60   -55

Ser Gly Gln Xaa Pro Glu Glu Ser Arg Ser Pro Ala Pro Pro Val Ala
            -50   -45   -40

Ser Arg Ser Gln Asn Arg Gly Tyr Arg Pro Trp His Gly Pro Leu Trp
        -35   -30   -25

Val His Gln Ser Val Arg Phe Gly Leu Tyr Ser Ile Leu His Phe Pro
    -20   -15   -10

Phe Trp Val His Gly Arg Xaa
-5   1

(2) INFORMATION FOR SEQ ID NO: 335:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 67 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -43..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.2
                                    seq PMQLLQVLSDVLA/EI

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro
        -40   -35   -30

Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Asp Ser Leu Glu Pro Met
        -25   -20   -15

Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys
    -10   -5   1   5

Val Arg Val Phe Ser Phe Phe Leu Met Gly Ser Arg Lys Pro Ile Ser
            10   15   20

Pro Ser Trp

(2) INFORMATION FOR SEQ ID NO: 336:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 110 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -104..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.1
                                    seq SSVASLTATPSLA/SP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Ser Pro Ser Cys Leu His Pro Asp Leu Trp Ser Met Cys Leu Glu
            -100   -95   -90

Val Pro Ser Phe Thr Ala Thr Asp Ser Val Asn Cys Gly Cys Cys Leu
            -85   -80   -75

Glu Leu Ala Thr Glu Pro Ala Arg Asn Ile Arg Ser Thr Thr Arg Ala
            -70   -65   -60

Ser Leu Leu Arg Cys Ser Ser Phe Thr Ser Thr Arg Asn Ser Thr Gly
        -55   -50   -45

Ile Ser Ala Leu Pro Pro Ala Ala Pro Met Ala Trp Pro Phe Ser Ala
-40   -35   -30   -25

Ser Leu Ser Thr Leu Pro Val Pro Leu Thr His Ser Ser Val Ala Ser
            -20   -15   -10

Leu Thr Ala Thr Pro Ser Leu Ala Ser Pro Thr Arg Met Met
            -5   1   5

(2) INFORMATION FOR SEQ ID NO: 337:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: -16..-1
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 5.1
                                 seq SFHLLLDPSSTQS/SI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Asp Leu Ser Phe His Leu Leu Leu Asp Pro Ser Ser Thr Gln Ser
    -15   -10   -5

Ser Ile Leu Lys His Leu Pro Cys
 1   5

(2) INFORMATION FOR SEQ ID NO: 338:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 53 amino acids
         (B) TYPE: AMINO ACID
         (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: -26..-1
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION: score 5
                                 seq VISVLILVGFGAC/IY

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Pro His Phe Leu Asp Trp Phe Val Xaa Val Tyr Leu Val Ile Ser
    -25   -20   -15

Val Leu Ile Leu Val Gly Phe Gly Ala Cys Ile Tyr Tyr Phe Glu Pro
-10   -5   1   5

Gly Leu Gln Glu Ala His Lys Trp Arg Met Xaa Arg Pro Trp Trp Thr
              10   15   20

Ala Thr Ser Thr Gly
        25

(2) INFORMATION FOR SEQ ID NO: 339:

```
      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 39 amino acids
           (B)  TYPE: AMINO ACID
           (D)  TOPOLOGY: LINEAR

     (ii)  MOLECULE TYPE: PROTEIN

     (vi)  ORIGINAL SOURCE:
           (A)  ORGANISM: Homo Sapiens
           (F)  TISSUE TYPE: Brain

    .(ix)  FEATURE:
           (A)  NAME/KEY: sig_peptide
           (B)  LOCATION: -30..-1
           (C)  IDENTIFICATION METHOD: Von Heijne matrix
           (D)  OTHER INFORMATION:  score 5
                             seq IVGLLAQLEKINA/EP

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 339:


Met Ser Lys Leu Lys Val Ile Pro Glu Lys Ser Leu Thr Asn Asn Ser
-30              -25             -20             -15

Arg Ile Val Gly Leu Leu Ala Gln Leu Glu Lys Ile Asn Ala Glu Pro
            -10             -5              1

Ser Glu Ser Asp Thr Ser Arg
          5




(2) INFORMATION FOR SEQ ID NO: 340:

      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 43 amino acids
           (B)  TYPE: AMINO ACID
           (D)  TOPOLOGY: LINEAR

     (ii)  MOLECULE TYPE: PROTEIN

     (vi)  ORIGINAL SOURCE:
           (A)  ORGANISM: Homo Sapiens
           (F)  TISSUE TYPE: Brain

     (ix)  FEATURE:
           (A)  NAME/KEY: sig_peptide
           (B)  LOCATION: -23..-1
           (C)  IDENTIFICATION METHOD: Von Heijne matrix
           (D)  OTHER INFORMATION:  score 5
                             seq LIPAMAFLSCVRP/ES

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 340:


Met Met Ser Ala Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala
          -20             -15             -10

Phe Leu Ser Cys Val Arg Pro Glu Ser Xaa Glu Pro Cys Val Glu Val
          -5              1               5
```

Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu
10   15   20

(2) INFORMATION FOR SEQ ID NO: 341:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 65 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -49..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.9
                                    seq VTVCCXLVAFLFC/IL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Asp Gly Thr Gln Leu Arg Gly Leu Thr Arg Met Tyr Gln Val
            -45   -40   -35

Pro Leu Xaa Leu Asp Arg Asp Glu Thr Leu Val Arg Leu Arg Phe Thr
            -30   -25   -20

Met Val Ala Leu Val Thr Val Cys Cys Xaa Leu Val Ala Phe Leu Phe
        -15   -10   -5

Cys Ile Leu Trp Ser Leu Leu Phe His Phe Lys Glu Thr Thr Ala Thr
    1   5   10   15

Gly

(2) INFORMATION FOR SEQ ID NO: 342:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 34 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -26..-1

            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.9
                                    seq LISMLQMLAVIIT/NT

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Lys Gln Asn Phe Leu Val Leu Asn Ser Val Trp Tyr Leu Ile Ser
    -25   -20   -15

Met Leu Gln Met Leu Ala Val Ile Ile Thr Asn Thr Thr Ile Thr Thr
-10   -5   1   5

Ile Gly

(2) INFORMATION FOR SEQ ID NO: 343:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 124 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -59..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.9
                                    seq LVEMCLEVLGSSA/GD

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Glu Cys Gln Asn Ser Ser Leu Lys Lys Cys Leu Leu Val Glu Lys
            -55   -50   -45

Ser Leu Val Lys Ala Ser Tyr Leu Ile Ala Phe Gln Thr Ala Ala Ser
            -40   -35   -30

Lys Lys Pro Phe Ser Ile Ala Glu Glu Leu Ile Lys Pro Tyr Leu Val
            -25   -20   -15

Glu Met Cys Leu Glu Val Leu Gly Ser Ser Ala Gly Asp Lys Met Lys
    -10   -5   1   5

Thr Ile Pro Leu Ser Asn Val Thr Ile Gln His Arg Ile Asp Glu Leu
                10   15   20

Ser Ala Asp Ile Glu Asp Gln Leu Ile Gln Lys Val Arg Glu Ser Lys
            25   30   35

Trp Phe Ala Leu Gln Ile Asp Glu Ser Ser Glu Ile Ser Asn Ile Thr
        40   45   50

Leu Leu Leu Cys Tyr Ile Arg Phe Ile Asp Tyr Asp
      55   60   65

(2) INFORMATION FOR SEQ ID NO: 344:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 27 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -23..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 4.8
                                  seq VMWLVALLEMCVC/KK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met His Ser Ser Ile Lys Thr Lys Gly Ser Val Met Trp Leu Val Ala
          -20   -15   -10

Leu Leu Glu Met Cys Val Cys Lys Lys Ser Arg
      -5   1

(2) INFORMATION FOR SEQ ID NO: 345:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 44 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -18..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 4.8
                                  seq LEAISSLSSFVLG/RM

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Thr Val Leu Pro Leu Glu Ala Ile Ser Ser Leu Ser Ser Phe Val
          -15   -10   -5

```
Leu Gly Arg Met Asn Ser Arg Gly Ala Gly Lys Thr Gln Asn Leu Asp
        1               5                   10

Ala Ser Ser Leu Leu Leu Leu Cys Cys Leu Ile Leu
15              20                  25
```

(2) INFORMATION FOR SEQ ID NO: 346:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 125 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -30..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.8
                              seq ILFCVGAVGACTL/SV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn
-30              -25               -20                   -15

Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val
            -10               -5                    1

Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr
        5               10              15

Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr
    20              25              30

Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu
35              40              45              50

Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg Glu Ala Leu
            55              60              65

Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp
            70              75              80

Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val
        85              90              95
```

(2) INFORMATION FOR SEQ ID NO: 347:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 46 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -25..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.8
                                    seq ALFYSVVVSTVSG/NE

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Asn Ser Ser Lys Glu Glu Met Arg Glu Leu Ala Ala Leu Phe Tyr
-25   -20   -15   -10

Ser Val Val Val Ser Thr Val Ser Gly Asn Glu Leu Lys Ser Met Ile
                -5   1   5

Glu Gln Leu Ile Lys Thr Thr Lys Asp Asn His Ser Leu Arg
        10   15   20

(2) INFORMATION FOR SEQ ID NO: 348:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 81 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -52..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.7
                                    seq LLAKALHLLKSSC/AP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
        -50   -45   -40

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn
    -35   -30   -25

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu

```
-20                    -15                 -10                    -5

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
                1               5                 10

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Ser
        15                  20                  25

Gly
```

(2) INFORMATION FOR SEQ ID NO: 349:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 47 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -29..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.7
                          seq LCYLSIFCLGVLF/II

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

```
Met Pro Cys Ile Ser Leu Leu Gly Leu Leu Tyr Asn Phe Val Gln Val
            -25                 -20                 -15

Leu Cys Tyr Leu Ser Ile Phe Cys Leu Gly Val Leu Phe Ile Ile Glu
        -10                 -5                      1

Arg Gly Ser Leu Lys Val Ser Lys Leu Ile Cys Arg Pro Pro Gly
    5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 350:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 47 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide

```
            (B) LOCATION: -15..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.7
                                    seq IAVLFCFFLLIIF/QT

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:


Met Lys Ile Ala Val Leu Phe Cys Phe Phe Leu Leu Ile Ile Phe Gln
-15               -10               -5                         1


Thr Asp Phe Gly Lys Asn Glu Glu Ile Pro Arg Lys Gln Arg Arg Lys
             5                  10                  15


Ile Tyr His Arg Arg Leu Arg Lys Ser Ser Thr Ser His Lys Gln
         20                  25                  30




(2) INFORMATION FOR SEQ ID NO: 351:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 48 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -43..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.7
                                    seq STWSSASLRGSWQ/QG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:


Met Ala Lys Gln Lys Pro His Val Leu Gly Ser Arg Val Met Pro Ala
         -40               -35               -30


Ser Cys Val Ser Glu Arg Arg Arg Lys Pro Ser Phe Gln Val Ser Thr
         -25               -20               -15


Trp Ser Ser Ala Ser Leu Arg Gly Ser Trp Gln Gln Gly Met Pro Gly
         -10               -5                1                  5




(2) INFORMATION FOR SEQ ID NO: 352:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN
```

```
(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Homo Sapiens
     (F) TISSUE TYPE: Brain

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: -15..-1
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:   score 4.6
                              seq FLYLKSVFDVSLG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:
```

```
Met Gly Phe Leu Tyr Leu Lys Ser Val Phe Asp Val Ser Leu Gly Ala
-15             -10                 -5                      1

Arg
```

```
(2) INFORMATION FOR SEQ ID NO: 353:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: -61..-1
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:   score 4.6
                                  seq LLLLHGGGHSALS/WA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:
```

```
Met Arg Met Gly Pro Gly Arg Lys Arg Asp Phe Ser Pro Val Pro Trp
   -60             -55                 -50

Ser Gln Tyr Phe Glu Ser Met Glu Asp Val Glu Val Glu Asn Glu Thr
-45             -40                 -35                      -30

Gly Lys Asp Thr Phe Arg Val Tyr Lys Ser Gly Ser Glu Gly Pro Val
                -25                 -20                      -15

Leu Leu Leu Leu His Gly Gly Gly His Ser Ala Leu Ser Trp Ala Val
                -10                 -5                       1

Phe Thr Ala Ala Xaa
    5
```

(2) INFORMATION FOR SEQ ID NO: 354:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -13..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.6
                                   seq MIFLLYLLPSSEE/RR

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ile Phe Leu Leu Tyr Leu Leu Pro Ser Ser Glu Glu Arg Arg Lys
        -10   -5   1

Leu Leu Phe Ser Pro His Arg
    5   10

(2) INFORMATION FOR SEQ ID NO: 355:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 70 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -61..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.6
                                   seq LLLLHGGGHSALS/WA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Arg Met Gly Pro Gly Arg Lys Arg Asp Phe Ser Pro Val Pro Trp
   -60   -55   -50

Ser Gln Tyr Phe Glu Ser Met Glu Asp Val Glu Val Glu Asn Glu Thr
  -45   -40   -35   -30

Gly Lys Asp Thr Phe Arg Val Tyr Lys Ser Gly Ser Glu Gly Pro Val
        -25   -20   -15

Leu Leu Leu Leu His Gly Gly Gly His Ser Ala Leu Ser Trp Ala Val
        -10   -5   1

Phe Thr Ala Ala Thr Trp
        5

(2) INFORMATION FOR SEQ ID NO: 356:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -16..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.5
                                    seq LLNLISILASIPS/QF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Leu Ser Leu Leu Asn Leu Ile Ser Ile Leu Ala Ser Ile Pro Ser
    -15   -10   -5

Gln Phe Lys Pro Gln Phe Ser Lys Leu Pro Leu Ser Gly Arg
  1   5   10

(2) INFORMATION FOR SEQ ID NO: 357:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 28 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -25..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.5
                                    seq LMLLWPVHPLLVG/HR

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Gly Thr Thr Ser Asn Met Val Thr Thr Ile His Leu Met Leu Leu
-25   -20   -15   -10

Trp Pro Val His Pro Leu Leu Val Gly His Arg Gly
                 -5   1

(2) INFORMATION FOR SEQ ID NO: 358:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 147 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -101..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 4.4
                                     seq ISHILAFFAASDG/IV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Gly Asp Pro Glu Arg Pro Glu Ala Ala Gly Leu Asp Gln Asp Glu
    -100   -95   -90

Arg Ser Ser Ser Asp Thr Asn Glu Ser Glu Ile Lys Ser Asn Glu Glu
-85   -80   -75   -70

Pro Leu Leu Arg Lys Ser Ser Arg Arg Phe Val Ile Phe Pro Ile Gln
             -65   -60   -55

Tyr Pro Asp Ile Trp Lys Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp
             -50   -45   -40

Thr Ala Glu Glu Val Asp Leu Ser Lys Asp Leu Pro His Trp Asn Lys
        -35   -30   -25

Leu Lys Ala Asp Glu Lys Tyr Phe Ile Ser His Ile Leu Ala Phe Phe
    -20   -15   -10

Ala Ala Ser Asp Gly Ile Val Asn Glu Asn Leu Val Glu Arg Phe Ser
 -5   1   5   10

Gln Glu Val Gln Val Pro Glu Ala Arg Cys Phe Tyr Gly Phe Gln Ile
            15   20   25

Leu Ile Glu Asn Val His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr
        30   35   40

```
Tyr Ile Arg
     45
```

(2) INFORMATION FOR SEQ ID NO: 359:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 65 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

     (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -16..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.4
                          seq GLFSLLPHPPCVG/RV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```
Met Asp Ala Gly Leu Phe Ser Leu Leu Pro His Pro Pro Cys Val Gly
    -15              -10              -5

Arg Val Leu Pro Gln Ser Arg Tyr His Leu His Pro Arg Ser Pro Leu
 1            5              10              15

Val Glu Asp Thr Cys Phe Phe Gln Arg Leu Lys Lys Ile Leu Asn Lys
            20              25              30

Ile Gly Asn Leu Phe His Ser Thr Lys Ser Leu Cys Val Ser Leu Ala
        35              40              45

Pro
```

(2) INFORMATION FOR SEQ ID NO: 360:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

     (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -14..-1

```
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 4.4
                                   seq LITLTYLIQGESA/RT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:


Met Leu Ile Thr Leu Thr Tyr Leu Ile Gln Gly Glu Ser Ala Arg Thr
          -10                 -5                  1

Thr Phe Glu
      5




(2) INFORMATION FOR SEQ ID NO: 361:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 31 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -26..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 4.4
                                   seq RVQCLCAIPFAFS/LT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:


Met Tyr Thr Gly Phe Arg Ile Glu Ala Thr Leu Leu Thr Arg Val Gln
   -25                 -20                 -15

Cys Leu Cys Ala Ile Pro Phe Ala Phe Ser Leu Thr Gly Ile Arg
-10                 -5                  1                 5




(2) INFORMATION FOR SEQ ID NO: 362:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 56 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
```

```
                (B) LOCATION: -47..-1
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION:   score 4.4
                                        seq ISHILAFFAASDG/IV
```

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:


```
Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp Thr Ala Glu Glu Val Asp
        -45             -40             -35

Leu Ser Lys Asp Leu Pro His Trp Asn Lys Leu Lys Ala Asp Glu Lys
        -30             -25             -20

Tyr Phe Ile Ser His Ile Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile
-15             -10             -5                      1

Val Asn Glu Asn Leu Val Glu Arg
            5
```


(2) INFORMATION FOR SEQ ID NO: 363:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 48 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -28..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.3
                                    seq FLGLAAMASPSRN/SQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:


```
Met Leu Leu His Leu Cys Ser Val Lys Asn Leu Tyr Gln Asn Arg Phe
        -25             -20             -15

Leu Gly Leu Ala Ala Met Ala Ser Pro Ser Arg Asn Ser Gln Ser Arg
        -10             -5                      1

Arg Arg Cys Lys Glu Pro Leu Arg Tyr Ser Tyr Asn Pro Asp Gln Gly
 5               10              15                      20
```


(2) INFORMATION FOR SEQ ID NO: 364:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 55 amino acids
            (B) TYPE: AMINO ACID

```
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -18..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.3
                                seq WTCLKSFPSPTSS/HA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:


Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro Thr
        -15             -10              .            -5

Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg Leu
        1                 5                  10

Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala Leu
15                  20                 25                    30

Gln Gly Thr Leu Thr Arg Gln
                35



(2) INFORMATION FOR SEQ ID NO: 365:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 73 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -33..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.3
                                seq LLGWGLNLTLGQG/AP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:


Met Glu Asp Leu Phe Ser Pro Ser Ile Xaa Pro Pro Ala Pro Asn Ile
        -30             -25              Pro         -20

Ser Val Pro Ile Leu Leu Gly Trp Gly Leu Asn Leu Thr Leu Gly Gln
        -15             -10                  .        -5
```

```
Gly Ala Pro Ala Ser Gly Pro Pro Ser Arg Arg Val Arg Leu Val Phe
 1               5               10              15

Leu Gly Val Ile Leu Val Val Ala Val Ala Xaa Asn Thr Thr Val Leu
            20              25              30

Cys Arg Leu Cys Gly Gly Gly Gly Pro
            35              40
```

(2) INFORMATION FOR SEQ ID NO: 366:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 55 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -52..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                             seq VMLETCGLLVSLG/HP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
        -50             -45             -40

Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
    -35             -30             -25

Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
-20             -15             -10                         -5

Val Ser Leu Gly His Pro Arg
             1
```

(2) INFORMATION FOR SEQ ID NO: 367:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -13..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION:  score 4.1
                                  seq MLILSQNIAQLEA/QV

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:


Met Leu Ile Leu Ser Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu
         -10                   -5                    1

Lys Val Thr Lys Glu Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Asn
     5                10                  15

Ser Lys Pro Ala Gly Phe Ser Gly Lys Trp Met Ser Gln
20                   25                  30



(2) INFORMATION FOR SEQ ID NO: 368:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 97 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

     (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -21..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION:  score 4.1
                                  seq GLWAHSWTCSCSA/AX

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:


Met Leu Leu Gly Ala Ser Ala Gln Gly Leu Trp Ala His Ser Trp Thr
    -20                 -15                 -10

Cys Ser Cys Ser Ala Ala Xaa Arg Ser Val His Pro Gly Gly Asp Trp
 -5                   1             5                    10

Met Gln Gln Phe Gln Ala Gly Phe Leu Pro Pro Gln Val Pro Ala His
            15                  20                  25

Leu Ser Leu Thr Trp Asp Val Ser Leu Leu Pro Pro Cys Leu Val Pro
        30                  35                  40

Lys Ala Leu Glu Phe Val Val His Phe Leu Lys Asn Asp Ile Phe Tyr
    45                  50                  55

Leu Thr Gln Tyr Ile Lys Asn Val Ile Ser Glu Cys Thr Phe Ser Phe
60                  65                  70                  75
```

Phe

(2) INFORMATION FOR SEQ ID NO: 369:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -15..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                          seq APLELSCWGGGWG/LP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:


```
Met Ala Ala Pro Leu Glu Leu Ser Cys Trp Gly Gly Gly Trp Gly Leu
-15               -10               -5                         1

Pro Ser Val His Ser Glu Ser Leu Val Val Met Ala Tyr Ala Lys Phe
              5                   10                  15

Ser Gly Ala Pro Leu Lys Val Asn Val Ile Asp Asn Thr Trp Arg Gly
          20              25              30

Ser Arg Gly Asp Val Pro Ile Leu Thr Thr Glu Asp Asp Met Val Ser
    35              40              45

Gln Pro Ala Arg
 50
```


(2) INFORMATION FOR SEQ ID NO: 370:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -20..-1

        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                                 seq LGFLNCYIAVARS/GG

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Ser Xaa Val Gly Ile Asp Leu Gly Phe Leu Asn Cys Tyr Ile Ala
-20   -15   -10   -5

Val Ala Arg Ser Gly Gly Ile Glu Thr Ile Ala Asn Glu Tyr Ser Asp
                 1   5   10

Arg Cys Thr Pro Ala Cys Ile Ser Leu Gly Ser Arg Thr Arg Ala Ile
        15   20   25

Gly Asn Ala Ala Lys Ser Gln Ile Val Thr Asn Val Arg Asn Thr Ile
    30   35   40

His Gly Phe Lys Lys
45

(2) INFORMATION FOR SEQ ID NO: 371:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 43 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -19..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.1
                                     seq FVVFSTMFTASSP/GE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Glu Tyr Ser Lys Xaa Phe Val Val Phe Ser Thr Met Phe Thr Ala
             -15   -10   -5

Ser Ser Pro Gly Glu Asp Phe Pro Pro Phe Phe Ser Gln Met Xaa Arg
             1   5   10

Leu Ser Arg Asn Tyr Phe Pro Cys Pro Pro Xaa
    15   20

(2) INFORMATION FOR SEQ ID NO: 372:

        (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 72 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -40..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.1
                               seq LPFRLPWASTATA/RC

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Pro Met Ala Ser Ser Pro Pro Pro Ser Pro His Pro Gln Glu Pro
-40   -35   -30   -25

Ala Pro Leu Leu Pro Ser Leu Pro Arg Leu Ser Leu Pro Phe Arg Leu
            -20   -15   -10

Pro Trp Ala Ser Thr Ala Thr Ala Arg Cys Pro Pro Ser Pro Leu Gly
            -5   1   5

Ser Leu Xaa Leu Met Leu Cys Ile Pro Thr Gly Phe Thr Pro Thr Gln
    10   15   20

Pro Arg Ala Pro Arg Pro Pro Gly
25   30

(2) INFORMATION FOR SEQ ID NO: 373:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 55 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -38..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4
                                   seq WALGLKFLSSSSQ/NF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Gln His Val Xaa Gly His Xaa Pro Asp Pro Ile Ala Ile Met Tyr

```
          -35                    -30                    -25
Val Cys Pro Pro Cys Gly His Thr Thr Trp Ala Leu Gly Leu Lys Phe
          -20                    -15             -10

Leu Ser Ser Ser Ser Gln Asn Phe Cys Ala Pro Val Leu Phe Leu Ile
          -5                  1             5                      10

Leu His Thr Gly Gly Gln Arg
                    15
```

(2) INFORMATION FOR SEQ ID NO: 374:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 53 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -30..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4
                        seq AGFLKCLLLSSLQ/SY

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

```
Met Gly Trp Glu Met Thr Cys Ile Lys Ser Phe Phe Trp Ala Arg Ser
-30                 -25                 -20                 -15

His Ala Gly Phe Leu Lys Cys Leu Leu Leu Ser Ser Leu Gln Ser Tyr
              -10                 -5                      1

Lys Glu Ala Ala Val Ile Phe Pro Leu Thr Asp Leu Leu Lys Leu Lys
        5                   10              15

Asp Tyr Gly Glu Trp
    20
```

(2) INFORMATION FOR SEQ ID NO: 375:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

          (F) TISSUE TYPE: Brain

     (ix) ·FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -36..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4
                                    seq VQLSFAATTPVLA/DK

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile Ala Glu
    -35   -30   -25

Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala Thr Thr
-20   -15   -10   -5

Pro Val Leu Ala Asp Lys
                1

(2) INFORMATION FOR SEQ ID NO: 376:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -16..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4
                                    seq ITWSLLFLYQCSL/HF

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met His Phe Ile Thr Trp Ser Leu Leu Phe Leu Tyr Gln Cys Ser Leu
    -15   -10   -5

His Phe Ile Ile Ile Lys Ala Gly
 1   5

(2) INFORMATION FOR SEQ ID NO: 377:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 41 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -36..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 3.9
                                  seq CWPSVASPSSSWS/SP

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Ser Gly Ala Ser Pro Ile Glu Arg Thr Pro Met Glu Glu Ala Pro
    -35   -30   -25

Ser Ser Cys Pro Thr Ser Ser Cys Trp Pro Ser Val Ala Ser Pro Ser
-20   -15   -10   -5

Ser Ser Trp Ser Ser Pro Trp Ala Ser
                1   5

(2) INFORMATION FOR SEQ ID NO: 378:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -37..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 3.9
                                  seq PGPSLRLFSGSQA/SV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
    -35   -30   -25

Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
    -20   -15   -10

Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5   1   5   10

Gln Glu

(2) INFORMATION FOR SEQ ID NO: 379:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 67 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -60..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                        seq AKVVSLSLQTSSA/HH

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```
Met Ile Ala Phe Phe Asp Glu Asp Asn Pro Arg Lys Arg Arg Ser Tyr
-60              -55              -50              -45

Ser Phe Thr Gln Ser Ala Gly Ile Leu Cys Gln Glu Thr Thr Tyr Ser
            -40              -35              -30

Thr Pro His Thr Lys Leu Glu Lys Ala Lys Ser Pro Thr Ala Asp Ala
            -25              -20              -15

Lys Val Val Ser Leu Ser Leu Gln Thr Ser Ser Ala His His Arg Gly
        -10              -5               1

Gly Xaa Gly
  5
```

(2) INFORMATION FOR SEQ ID NO: 380:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 87 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -48..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                        seq ALFCTLPCPVERG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Gly Lys Ser Ile Xaa Ser Leu Cys Ser Val Xaa Leu Lys Ala Arg
        -45   -40   -35

Leu Lys Gly Xaa Leu Glu Ala Val His Leu Cys Leu Arg Ala Gln Lys
        -30   -25   -20

Arg Arg Thr Ala Leu Phe Cys Thr Leu Pro Cys Pro Val Glu Arg Gly
        -15   -10   -5

Gln Gln Val Pro Gly Xaa Xaa Xaa Arg Leu Arg Leu Ala Ser Pro Ser
 1   5   10   15

Val Ala Lys Val Phe Gln Cys Phe Leu Ser Lys Leu Cys Val Trp Asn
          20   25   30

Ile Lys Asp Gly Leu Ser Arg
         35

(2) INFORMATION FOR SEQ ID NO: 381:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 53 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: -15..-1
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 3.9
                                         seq LHMTLFRVPFTFS/XF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Cys Leu His Met Thr Leu Phe Arg Val Pro Phe Thr Phe Ser Xaa
-15   -10   -5   1

Phe Trp Lys Gly Ala Gly Arg Gln Glu Glu Cys Ser Phe Lys Pro Ser
          5   10   15

Leu Tyr Tyr Tyr Lys Leu Ile Met Val Leu Lys Ile Ala Leu Leu Leu
         20   25   30

Ser Pro Pro Pro Lys
         35

(2) INFORMATION FOR SEQ ID NO: 382:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -14..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.9
                                  seq LNILKTLTSAALP/SP

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Leu Asn Ile Leu Lys Thr Leu Thr Ser Ala Ala Leu Pro Ser Pro
            -10   -5   1

Ser Pro Arg Pro Asn Lys Arg
         5

(2) INFORMATION FOR SEQ ID NO: 383:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 51 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -40..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.9
                                  seq SPLLCLYHPPVYT/ST

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Arg Ala Arg Val Trp Pro Arg Ser His Gly Ile Pro Val Pro Ser
-40   -35   -30   -25

Phe Leu Ser Lys Ser Ser Leu Ser His Thr Pro Ser Pro Leu Leu Cys
            -20   -15   -10

Leu Tyr His Pro Pro Val Tyr Thr Ser Thr Thr Thr Pro Ser Ile Pro

                    -5   1   5

Pro Arg Leu
    10

(2) INFORMATION FOR SEQ ID NO: 384:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 51 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -36..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.9
                                    seq SLCLSLLIPGPKP/LV

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Trp Asn Ala Val Ala Ile Ile Cys Asn Gly Ser Trp Cys Gln Thr
    -35   -30   -25

Xaa Ser Thr Ser Gly Leu Glu Ser Leu Cys Leu Ser Leu Leu Ile Pro
-20   -15   -10   -5

Gly Pro Lys Pro Leu Val Ser Val Gly Ile Asn Gln Leu Leu Leu Thr
                1   5   10

Ser Ser Arg
        15

(2) INFORMATION FOR SEQ ID NO: 385:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -14..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix

          (D) OTHER INFORMATION: score 3.9
                                    seq LRLGLFKISWARC/LS

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Leu Arg Leu Gly Leu Phe Lys Ile Ser Trp Ala Arg Cys Leu Ser
              -10   -5   1

Tyr Ser Lys Thr Gln Xaa Glu
          5

(2) INFORMATION FOR SEQ ID NO: 386:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 61 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -36..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.9
                                     seq VVEILPYLPCLTA/RD

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
   -35   -30   -25

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
-20   -15   -10   -5

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
              1   5   10

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr
          15   20   25

(2) INFORMATION FOR SEQ ID NO: 387:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 40 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:

        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -36..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.8
                                seq GTDSLSFLPPCPC/CP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Pro Gly Ser Ser Gly Leu Arg Phe Ile Cys Lys Ser Arg Asn His
    -35   -30   -25

Pro Gln Phe Gly Ser Phe Ser Gly Thr Asp Ser Leu Ser Phe Leu Pro
-20   -15   -10   -5

Pro Cys Pro Cys Cys Pro Ala Ala
                1

(2) INFORMATION FOR SEQ ID NO: 388:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        .(A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -57..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.8
                                seq QLXLVMEFCGAGS/VT

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile Asn
    -55   -50   -45

Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr Gly
    -40   -35   -30

Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Xaa Leu
-25   -20   -15   -10

Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys Asn
                -5   1   5

Thr Gly

(2) INFORMATION FOR SEQ ID NO: 389:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -24..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.8
                          seq KLFLVFLLNICKG/IV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ile Phe Gly Leu Tyr Phe Val Leu Ala Val Lys Leu Phe Leu Val
          -20   -15   -10

Phe Leu Leu Asn Ile Cys Lys Gly Ile Val
        -5   1

(2) INFORMATION FOR SEQ ID NO: 390:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 amino acids
        (B) TYPE: AMINO ACID
      . (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -34..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                          seq IKCSSWISSLASG/IP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Lys Lys Arg Val Glu Glu Leu Ile Val Phe Pro Gly Glu Val
          -30   -25   -20

Thr Ser Phe Ser Ser Ile Lys Cys Ser Ser Trp Ile Ser Ser Leu Ala
        -15   -10   -5

```
Ser Gly Ile Pro His Ser Leu Gly Phe Ser Leu Pro Pro Gly
     1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 391:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 57 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -28..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                                  seq ACLFSXFLAVSRH/PN

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```
Met Pro Ser Ser Ser Leu Ala Glu Leu Cys Leu Met Gln Gln Asp Ala
        -25              -20              -15

Cys Leu Phe Ser Xaa Phe Leu Ala Val Ser Arg His Pro Asn Tyr Xaa
    -10              -5                   1

Cys Ser Ile Ser Thr Lys Gly Glu Val Arg Glu Lys Leu Val Pro Trp
 5               10              15                   20

Ile Thr His Gln Met Ala Arg Met Leu
            25
```

(2) INFORMATION FOR SEQ ID NO: 392:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -40..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6

seq LQMRMQLPCLVLG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```
Met Asp Leu Trp Ser Cys Leu Phe Pro Val Met Leu Met Glu Pro Ser
-40              -35              -30                          -25

Lys Gly Leu Glu Asp Ser Glu Trp Lys Met Ala Leu Gln Met Arg Met
                -20              -15                      -10

Gln Leu Pro Cys Leu Val Leu Gly Glu Glu Gln Thr Leu Gly
          -5                    1              5
```

(2) INFORMATION FOR SEQ ID NO: 393:

          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 37 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

          (ii) MOLECULE TYPE: PROTEIN

          (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

          (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: -27..-1
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION: score 3.6
                                      seq AVPLPTTSTLTSA/ST

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```
Met Ser Gly Lys Gly Lys Cys Arg Pro Ile Ala Leu Arg Arg Ala Val
    -25              -20                  -15

Pro Leu Pro Thr Thr Ser Thr Leu Thr Ser Ala Ser Thr Gly Phe Leu
    -10              -5                    1              5

Trp Ile Leu Lys Glu
              10
```

(2) INFORMATION FOR SEQ ID NO: 394:

          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

          (ii) MOLECULE TYPE: PROTEIN

          (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens

    (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -18..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                            seq IQKSSGLFCPSQA/QS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Thr Pro Lys Ala Ile Gln Lys Ser Ser Gly Leu Phe Cys Pro Ser
        -15   -10   -5

Gln Ala Gln Ser Ala Arg Pro Ala Glu Lys
        1   5

(2) INFORMATION FOR SEQ ID NO: 395:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 103 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -72..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.6
                            seq CTSLLQLYDASNS/EW

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Pro Asp Gln Phe Asp Gln Ala Val Val Leu Asn Gln Leu Arg Tyr
        -70   -65   -60

Ser Gly Met Leu Glu Thr Val Arg Ile Arg Lys Ala Gly Tyr Ala Val
        -55   -50   -45

Arg Arg Pro Phe Gln Asp Phe Tyr Lys Arg Tyr Lys Val Leu Met Arg
-40   -35   -30   -25

Asn Leu Ala Leu Pro Glu Asp Val Arg Gly Lys Cys Thr Ser Leu Leu
            -20   -15   -10

Gln Leu Tyr Asp Ala Ser Asn Ser Glu Trp Gln Leu Gly Lys Thr Lys
        -5   1   5

Val Phe Leu Arg Glu Ser Leu Glu Gln Lys Leu Glu Lys Arg Arg Glu
    10   15   20

Glu Glu Val Ser His Ala Gly
 25   30

(2) INFORMATION FOR SEQ ID NO: 396:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -15..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.6
                                     seq LVSFFLELNVLQQ/WP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Cys Leu Val Ser Phe Phe Leu Glu Leu Asn Val Leu Gln Gln Trp
-15   -10   -5   1

Pro Ala Gly

(2) INFORMATION FOR SEQ ID NO: 397:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 44 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -13..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.6
                                     seq MRSLACLTPCGHA/GS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Arg Ser Leu Ala Cys Leu Thr Pro Cys Gly His Ala Gly Ser Arg
              -10   -5   1

```
Leu Gln Ser Ser Leu Ser Lys Tyr Leu Val Leu Pro Asn Leu Glu Cys
        5               10              15

Leu Phe Phe Leu Phe Leu Ile Ser Asn Arg Arg Trp
20              25              30
```

(2) INFORMATION FOR SEQ ID NO: 398:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 82 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -13..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.5
                                    seq MHLLSNWANPASS/RR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

```
Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
        -10                 -5                  1

Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
        5               10              15

Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
20              25              30                      35

Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
            40              45              50

Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
            55              60              65

Arg Arg
```

(2) INFORMATION FOR SEQ ID NO: 399:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 118 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens

        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -24..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                            seq FAMLHSVWRLIPA/FR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Trp Ser Gly Lys Trp Ala Leu Val Ser Pro Phe Ala Met Leu His
            -20   -15   -10

Ser Val Trp Arg Leu Ile Pro Ala Phe Arg Gly Tyr Ala Gln Gln Asp
            -5   1   5

Ala Gln Glu Phe Leu Cys Glu Leu Leu Asp Lys Ile Gln Arg Glu Leu
    10   15   20

Glu Thr Thr Gly Thr Ser Leu Pro Ala Leu Ile Pro Thr Ser Gln Arg
 25   30   35   40

Lys Leu Ile Lys Gln Val Leu Asn Val Val Asn Asn Ile Phe His Gly
            45   50   55

Gln Leu Leu Ser Gln Val Thr Cys Leu Ala Cys Asp Asn Lys Ser Asn
        60   65   70

Thr Ile Glu Pro Phe Trp Asp Leu Ser Leu Glu Xaa Pro Glu Arg Tyr
    75   80   85

Gln Cys Ser Xaa Lys Gly
    90

(2) INFORMATION FOR SEQ ID NO: 400:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 41 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -20..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                            seq KFCLICLLTFIFH/HC

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

```
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
-20              -15              -10                      -5

Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
             1               5               10

Pro Glu Ala Leu His Arg Gln Gln Gly
        15                  20
```

(2) INFORMATION FOR SEQ ID NO: 401:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 49 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -24..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                            seq ALSLFYTADTSHG/SE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

```
Met Gly Arg Arg His Trp Val Leu Thr His Ser Ala Leu Ser Leu Phe
            -20              -15              -10

Tyr Thr Ala Asp Thr Ser His Gly Ser Glu Lys Pro Tyr Leu Ser Leu
            -5               1               5

Phe Gly Arg Glu Gly Gly Arg Glu Gly Ser Asn Pro Lys Tyr Tyr Ser
    10                  15                  20

Phe
25
```

(2) INFORMATION FOR SEQ ID NO: 402:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 93 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -16..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 12.5
                                   seq FVVLLALVAGVLG/NE

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:
```

```
Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly
    -15             -10             -5
```

```
Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn
  1           5               10                      15
```

```
Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
            20              25                  30
```

```
Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
            35              40                  45
```

```
Val Gly Asn Leu Phe His Arg Pro Arg Ala Ser Val Met Val Met Val
        50              55              60
```

```
Lys Gly Val Asn Asn Xaa Pro Leu Pro Pro Xaa Trp Xaa
 65              70              75
```

```
(2) INFORMATION FOR SEQ ID NO: 403:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 65 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -16..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 10.1
                                     seq LLLQLAVLGAALA/AA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:
```

```
Met Ala Pro Leu Leu Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala
    -15             -10             -5
```

```
Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr
  1           5               10                      15
```

```
Lys Met Pro Ala Leu His Arg His Glu Glu Glu Lys Phe Phe Leu Asn
            20              25                  30
```

Ala Lys Gly Gln Lys Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr
        35   40   45

Arg

(2) INFORMATION FOR SEQ ID NO: 404:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 84 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -50..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 9.8
                                    seq LLRLLQLVSTCVA/FS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser
-50   -45   -40   -35

Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu
        -30   -25   -20

Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
        -15   -10   -5

Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
        1   5   10

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
 15   20   25   30

Ile Ile Leu Ile

(2) INFORMATION FOR SEQ ID NO: 405:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 72 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens

            (F) TISSUE TYPE: Brain

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -18..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 9.2
                                    seq VFLCSLLAPMVLA/SA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val
        -15   -10   -5

Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr
         1   5   10

Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu
 15   20   25   30

Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser
            35   40   45

Phe Asn Gln Lys Pro Arg Asn Arg
        50

(2) INFORMATION FOR SEQ ID NO: 406:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 70 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -46..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.9
                                    seq LLGLLSAEQLAEA/SV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu
    -45   -40   -35

Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val
-30   -25   -20   -15

Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val
            -10   -5   1

Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu
        5   10   15

Glu Met Lys Ser Leu Ile
    20

(2) INFORMATION FOR SEQ ID NO: 407:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 57 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -47..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.9
                                    seq LLLPRVLLTMASG/SP

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser
        -45   -40   -35

Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser
    -30   -25   -20

Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
-15   -10   -5   1

Pro Pro Thr Gln Pro Ser Pro Ala Trp
        5   10

(2) INFORMATION FOR SEQ ID NO: 408:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 92 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -40..-1

```
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 7.9
                                    seq SLLLLFGGQFASS/QE


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:


Met Ala Leu Ser Cys Thr Leu Asn Arg Tyr Leu Leu Leu Met Ala Gln
-40               -35           -30               -25

Glu His Leu Glu Phe Arg Leu Pro Glu Ile Xaa Ser Leu Leu Leu Leu
            -20           -15           -10

Phe Gly Gly Gln Phe Ala Ser Ser Gln Glu Thr Tyr Gly Lys Ser Pro
            -5                1               5

Phe Trp Ile Leu Ser Ile Pro Ser Glu Asp Ile Ala Arg Asn Leu Met
    10              15              20

Lys Arg Thr Val Cys Ala Lys Ser Ile Phe Glu Leu Trp Gly His Gly
    25              30              35              40

Gln Ser Pro Glu Glu Leu Tyr Ser Ser Leu Lys Asn
            45                50
```

(2) INFORMATION FOR SEQ ID NO: 409:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 91 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -53..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.1
                                    seq IAVGLGVAALAFA/GR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```
Met Ala Ala Arg Gly Val Ile Ala Pro Val Gly Glu Ser Leu Arg Tyr
            -50               -45           -40

Ala Glu Tyr Leu Gln Pro Ser Ala Lys Arg Pro Asp Ala Asp Val Asp
        -35           -30               -25

Gln Gln Arg Leu Val Arg Ser Leu Ile Ala Val Gly Leu Gly Val Ala
    -20               -15           -10

Ala Leu Ala Phe Ala Gly Arg Tyr Ala Phe Arg Ile Trp Lys Pro Leu
    -5                1           5               10
```

Glu Gln Val Ile Thr Glu Thr Ala Lys Lys Ile Ser Thr Pro Ser Phe
            15   20   25

Ser Ser Tyr Tyr Lys Gly Gly Phe Glu Arg Arg
        30   35

(2) INFORMATION FOR SEQ ID NO: 410:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -28..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.6
                                    seq VLGXLFLGGLCRG/WD

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Arg Met Cys Ala Gly Ser Ile Tyr Lys Ser Ala Thr Gln Ala Val
        -25   -20   -15

Leu Gly Xaa Leu Phe Leu Gly Gly Leu Cys Arg Gly Trp Asp Ala
        -10   -5   1

(2) INFORMATION FOR SEQ ID NO: 411:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 80 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -78..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.3
                                    seq TLIMLLSWQLSVS/SV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Ala Glu Arg Arg Arg Pro Leu Ser Pro Ile Pro Ser Xaa Arg Arg
             -75   -70   -65

Pro Ser Glu Pro Ser Arg Pro Arg Pro Ala Ala Ala Gly Xaa Arg Ser
             -60   -55   -50

Leu Pro Arg Pro Gly Asp Glu Glu Leu Gln Leu Pro Cys Ala Val His
    -45   -40   -35

Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly Phe Val Phe Gly
-30   -25   -20   -15

Thr Thr Leu Ile Met Leu Leu Ser Trp Gln Leu Ser Val Ser Ser Val
             -10   -5   1

(2) INFORMATION FOR SEQ ID NO: 412:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 133 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -109..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 6
                                seq LQLLLGMTASAVA/AL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Ala Ala Pro Val Leu Leu Arg Val Ser Val Pro Arg Trp Glu Arg
             -105   -100   -95

Val Ala Arg Tyr Ala Val Cys Ala Ala Gly Ile Leu Leu Ser Ile Tyr
             -90   -85   -80

Ala Tyr His Val Glu Arg Glu Lys Glu Arg Asp Pro Glu His Arg Ala
             -75   -70   -65

Leu Cys Asp Leu Gly Pro Trp Val Lys Cys Ser Ala Ala Leu Ala Ser
             -60   -55   -50

Arg Trp Gly Arg Gly Phe Gly Leu Leu Gly Ser Ile Phe Gly Lys Asp
-45   -40   -35   -30

Gly Val Leu Asn Gln Pro Asn Ser Val Phe Gly Leu Ile Phe Tyr Ile
             -25   -20   -15

Leu Gln Leu Leu Leu Gly Met Thr Ala Ser Ala Val Ala Ala Leu Ile

```
                -10                    -5                      1

Leu Met Thr Ser Ser Ile Met Ser Val Val Gly Ser Cys Thr Trp Pro
         5                   10                   15

Thr Phe Cys Thr Thr
 20
```

(2) INFORMATION FOR SEQ ID NO: 413:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 106 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

     (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -34..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.9
                         seq LGAAALALLLANT/DV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
             -30                -25                -20

Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala
             -15                -10                -5

Asn Thr Asp Val Phe Leu Ser Lys Pro Xaa Lys Ala Ala Leu Glu Tyr
         1                   5                   10

Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15                   20                  25                   30

Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
             35                  40                  45

Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
             50                  55                  60

Ser Leu Lys Ser Met Leu Asp Gln Leu Gly
             65                  70
```

(2) INFORMATION FOR SEQ ID NO: 414:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 56 amino acids
        (B) TYPE: AMINO ACID

          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -37..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.9
                              seq MLIMLGIFFNVHS/AV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
        -35   -30   -25

Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
    -20   -15   -10

Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
 -5   1   5   10

Lys Asp Phe Glu Asn Gly Pro Arg
              15

(2) INFORMATION FOR SEQ ID NO: 415:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 32 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

         (ii) MOLECULE TYPE: PROTEIN

         (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

         (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -20..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 4.9
                                  seq XSLFLHAVSSSFT/QL

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Ile Leu Pro Tyr Arg Met Xaa Ser Leu Phe Leu His Ala Val Ser
-20   -15   -10   -5

Ser Ser Phe Thr Gln Leu Arg Ser Cys Gln Gly Asp Arg Val Trp Arg
         1   5   10

(2) INFORMATION FOR SEQ ID NO: 416:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 78 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -63..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.8
                                seq LYTVRALAGRAWA/AV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Ala Thr Leu Val Glu Leu Pro Asp Ser Val Leu Leu Glu Ile Phe
          -60   -55   -50

Ser Tyr Leu Pro Val Arg Asp Arg Ile Arg Ile Ser Arg Val Cys His
      -45   -40   -35

Arg Trp Lys Arg Leu Val Asp Asp Arg Trp Leu Trp Arg His Val Asp
 -30   -25   -20

Leu Thr Leu Tyr Thr Val Arg Ala Leu Ala Gly Arg Ala Trp Ala Ala
-15   -10   -5   1

Val Ala Val Pro Gly Xaa Arg Arg Pro Pro Leu Pro Pro Trp
         5   10   15

(2) INFORMATION FOR SEQ ID NO: 417:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 92 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -41..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.7
                                seq LFSCFCFLSHKFG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Lys Asn Ala Cys Ile Val Leu Pro Pro Thr Pro Pro Pro Ser Leu
    -40   -35   -30

Gln Pro Ser Ala Ser Leu Leu Ala Pro Asn Arg Phe Leu Phe Ser Cys
-25   -20   -15   -10

Phe Cys Phe Leu Ser His Lys Phe Gly Lys Lys Val Ile Tyr Phe Asn
                -5   1   5

Tyr Leu Ser Glu Leu His Glu His Leu Lys Tyr Asp Gln Leu Val Ile
        10   15   20

Pro Pro Glu Val Leu Arg Tyr Asp Glu Lys Leu Gln Ser Leu His Glu
    25   30   35

Gly Arg Thr Pro Xaa Pro Thr Lys Thr Pro Pro Gly
40   45   50

(2) INFORMATION FOR SEQ ID NO: 418:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 55 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -28..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.6
                                    seq PLQWSLLVAVVAG/SV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
        -25   -20   -15

Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
        -10   -5   1

Tyr Gly Val Thr Arg Val Xaa Ser Glu Lys Cys Asn Asn Leu Trp Leu
5   10   15   20

Phe Leu Glu Thr Gly Leu Gly
                25

(2) INFORMATION FOR SEQ ID NO: 419:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -53..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.5
                          seq LLWTPLLSPGSLR/VI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Tyr Cys Lys Ile Leu Val Leu Met Leu His Thr Glu Leu Ile Arg
        -50   -45   -40

Thr Asp Tyr Ser Ser Val Asp Gln Leu Leu Leu Asn Tyr Pro Ala Glu
        -35   -30   -25

Glu Gly Leu Gly Arg Glu Arg Ser Leu Leu Trp Thr Pro Leu Leu Ser
    -20   -15   -10

Pro Gly Ser Leu Arg Val Ile Leu Glu Ser Arg Glu Val Pro Val Ser
 -5   1   5   10

Leu Trp Pro Gln Thr
        15

(2) INFORMATION FOR SEQ ID NO: 420:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 86 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -26..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.5
                          seq ENSLIILLQGLQG/RV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```
Met Ala Val Ser His Ser Val Lys Glu Arg Thr Ile Ser Glu Asn Ser
    -25             -20                 -15

Leu Ile Ile Leu Leu Gln Gly Leu Gln Gly Arg Val Thr Thr Val Asp
-10              -5                  1                   5

Leu Arg Asp Glu Ser Val Ala His Gly Arg Ile Asp Xaa Val Asp Ala
            10                  15              20

Phe Met Asn Ile Arg Leu Ala Lys Val Thr Tyr Thr Asp Arg Trp Gly
        25                  30              35

His Gln Val Lys Leu Asp Asp Leu Phe Val Thr Gly Arg Asn Val Arg
    40                  45                  50

Tyr Val His Ile Pro Asp
55                  60
```

(2) INFORMATION FOR SEQ ID NO: 421:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 91 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -23..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 4.4
                                      seq QFILLGTTSVVTA/AL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

```
Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
        -20             -15                 -10

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
        -5              1               5

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
10              15                  20                      25

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
                30                  35                  40

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
            45                  50                  55

Ser Gln Phe Val Glu Asn Cys Xaa Gly Val Arg
```

             60   65

(2) INFORMATION FOR SEQ ID NO: 422:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 142 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

        (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -139..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 4.3
                                     seq GILVPHSLRQAQA/SF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ala Ala Leu Asp Leu Arg Ala Xaa Trp Ile Arg Trp Ser Cys Ser
              -135   -130   -125

Cys Leu Gly Xaa Leu Xaa Gly Ala Gly Gly Glu Thr Asn Gly Val Glu
              -120   -115   -110

Arg Pro Gly Gly Gly Gly Leu Ala Leu Ala Arg Gln Gly Ser Leu Arg
              -105   -100   -95

Asp Gly Arg Gln Val Gly Arg Ala Pro Ala Val Cys Phe Pro His Gly
        -90   -85   -80

Ala Pro Gly Leu Pro Pro Arg Gln Arg Xaa Xaa Gly Gly Xaa Pro Glu
-75   -70   -65   -60

Val Gln Gly Gly Glu Ser Trp Cys Pro Arg Pro Arg Gly Gly Gly Ala
              -55   -50   -45

Ser Arg Thr Gly Leu Arg Arg Arg Lys Gly Pro Thr Lys Thr Pro Glu
              -40   -35   -30

Pro Glu Ser Ser Glu Ala Pro Gln Asp Pro Leu Asn Trp Phe Gly Ile
              -25   -20   -15

Leu Val Pro His Ser Leu Arg Gln Ala Gln Ala Ser Phe Arg
        -10   -5   1

(2) INFORMATION FOR SEQ ID NO: 423:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 29 amino acids
             (B) TYPE: AMINO ACID

```
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -21..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.1
                                    seq WWISLLPSLLSIC/KV

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:


Met Ala Phe Leu Pro Ser Pro Ala Trp Trp Ile Ser Leu Leu Pro Ser
    -20             -15             -10

Leu Leu Ser Ile Cys Lys Val Leu Met Pro Lys Leu Lys
 -5              1               5




(2) INFORMATION FOR SEQ ID NO: 424:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 127 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -49..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 3.8
                                    seq PAFHLPLPGPTLA/FL

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:


Met Glu Pro Lys Val Ala Glu Leu Lys Gln Lys Ile Glu Asp Thr Leu
            -45             -40             -35

Cys Pro Phe Gly Phe Glu Val Tyr Pro Phe Gln Val Ala Trp Tyr Asn
            -30             -25             -20

Glu Leu Leu Pro Pro Ala Phe His Leu Pro Leu Pro Gly Pro Thr Leu
        -15             -10              -5

Ala Phe Leu Val Leu Ser Thr Pro Ala Met Phe Asp Arg Ala Leu Lys
    1               5               10              15
```

```
Pro Phe Leu Gln Ser Cys His Leu Arg Met Leu Thr Asp Pro Val Asp
             20              25                  30

Gln Cys Val Ala Tyr His Leu Gly Arg Val Arg Glu Ser Leu Pro Glu
             35              40                  45

Leu Gln Ile Glu Ile Ile Ala Xaa Xaa Arg Gly Ala Pro Gln Pro Thr
             50              55                  60

Pro Gln Asp Pro Gly Pro Asp Ser Ser His Val Ala Gly Ala Ala
 65              70                  75
```

(2) INFORMATION FOR SEQ ID NO: 425:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 98 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -13..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.7
                                    seq MLVLRSGLTKALA/SR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

```
Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr
             -10              -5                  1

Leu Ala Pro Gln Val Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
  5                  10              15

Asp Gly Thr Phe Tyr Glu Phe Arg Thr Tyr Tyr Leu Lys Pro Ser Asn
 20              25              30                  35

Met Asn Ala Phe Met Glu Asn Leu Lys Lys Asn Ile His Leu Arg Thr
                 40              45                  50

Ser Tyr Ser Glu Leu Val Gly Phe Trp Ser Val Glu Phe Gly Gly Arg
             55              60                  65

Thr Asn Lys Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
         70              75                  80

Ala Glu
 85
```

(2) INFORMATION FOR SEQ ID NO: 426:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 27 amino acids
    (B) TYPE: AMINO ACID
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Brain

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: -23..-1
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION:  score 10.5
                            seq LLFVLLLFSLLPA/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:
```

Met Ser Gly Gly His Leu Ala Asp Leu Thr Leu Leu Phe Val Leu Leu
        -20   -15   -10

Leu Phe Ser Leu Leu Pro Ala Cys Leu Pro Arg
        -5   .   1

```
(2) INFORMATION FOR SEQ ID NO: 427:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 54 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -51..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 10.1
                                seq LLGALTLLGLVTS/FY

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:
```

Met Lys Pro Ser Arg Thr Pro Ala Arg Leu Trp Met Leu Pro Gln Gln
    -50   -45   -40

Gln Ala Gly Ala Val Val Val Ala Ala Pro Thr Glu Arg His Pro Thr
-35   -30   -25   -20

His His Met Ala Gly Trp Leu Leu Gly Ala Leu Thr Leu Leu Gly Leu
            -15   -10   -5

Val Thr Ser Phe Tyr Lys
                 1

(2) INFORMATION FOR SEQ ID NO: 428:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 131 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -64..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 9.5
                                      seq LSLLAALAHLAAA/EK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Gly Glu Ser Ile Pro Leu Ala Ala Pro Val Pro Val Glu Gln Ala
             -60   -55   -50

Val Leu Glu Thr Phe Phe Ser His Leu Gly Ile Phe Ser Tyr Asp Lys
             -45   -40   -35

Ala Lys Asp Asn Val Glu Lys Glu Arg Glu Ala Asn Lys Ser Ala Gly
         -30   -25   -20

Gly Ser Trp Leu Ser Leu Leu Ala Ala Leu Ala His Leu Ala Ala Ala
     -15   -10   -5

Glu Lys Val Tyr His Ser Leu Thr Tyr Leu Gly Gln Lys Leu Gly Gly
 1   5   10   15

Gln Ser Phe Phe Ser Arg Lys Asp Ser Ile Arg Thr Ile Tyr Thr Ser
         20   25   30

Leu His Asn Glu Leu Lys Lys Val Val Thr Gly Arg Gly Ala Xaa Xaa
         35   40   45

Trp Asp Cys Ser Ser Arg Gly Arg Thr Pro Phe Pro Pro Val Arg Ala
     50   55   60

Ala Tyr Gly
 65

(2) INFORMATION FOR SEQ ID NO: 429:

        (i) SEQUENCE CHARACTERISTICS:

```
           (A) LENGTH: 86 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -38..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION:  score 9.3
                                  seq QLLYLSLLSGLHG/QE

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:
```

```
Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr Gln Leu Leu Leu
        -35                 -30                 -25

Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu Tyr Leu Ser Leu
        -20                 -15                 -10

Leu Ser Gly Leu His Gly Gln Glu Glu Gln Asp Gln Tyr Phe Glu Phe
        -5                   1                 5                  10

Phe Pro Pro Ser Pro Arg Ser Val Asp Gln Val Lys Ala Gln Leu Arg
                15                 20                  25

Thr Ala Leu Ala Ser Gly Gly Val Leu Asp Ala Ser Gly Asp Tyr Arg
            30                 35                  40

Val Tyr Arg Gly His Gly
        45
```

```
(2) INFORMATION FOR SEQ ID NO: 430:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 26 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -24..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION:  score 9.1
                                  seq LFAFHLLLSFILG/SR

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:
```

Met Leu Arg Ala Glu Leu Lys Ile Ala Val Val Leu Phe Ala Phe His
            -20   -15   -10

Leu Leu Leu Ser Phe Ile Leu Gly Ser Arg
            -5   1

(2) INFORMATION FOR SEQ ID NO: 431:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 76 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -55..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 9
                                 seq LLILLLRTFLCSA/MI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Asn His Gln Gln Thr Leu Ile Gly Arg Leu Leu Cys Asp Leu His
-55   -50   -45   Cys   -40

Gly Leu Ser Leu Ser Pro Pro Val Ala Asn Asn Val Gln Ala Leu Phe
            -35   -30   -25

Arg Met Leu Thr Pro Glu Ala Tyr Ser Cys Leu Leu Ile Leu Leu Leu
            -20   -15   -10

Arg Thr Phe Leu Cys Ser Ala Met Ile Ala Asn Thr Leu His Leu Lys
            -5   1   5

Tyr His Leu Gln Leu Ile Asp Asn Ala Cys Pro Glu
10   15   20

(2) INFORMATION FOR SEQ ID NO: 432:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 84 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -40..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 8.6
                                 seq LFCVLGIVLLVTG/IV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe
-40   -35   -30   -25

Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu
        -20   -15   -10

Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr
        -5   1   5

Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala
    10   15   20

Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly
 25   30   35   40

Asn Arg Lys His

(2) INFORMATION FOR SEQ ID NO: 433:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 89 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -65..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 8.4
                                     seq LLWFIHLVFVVLX/LF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Ala Ala Gly Gly Arg Met Glu Asp Gly Ser Leu Asp Ile Thr Gln
-65   -60   -55   -50

Ser Ile Glu Asp Asp Pro Leu Leu Asp Ala Gln Leu Leu Pro His His
            -45   -40   -35

Ser Leu Gln Ala His Phe Arg Pro Arg Phe His Pro Leu Pro Thr Val

```
           -30                    -25                    -20
Ile Ile Val Asn Leu Leu Trp Phe Ile His Leu Val Phe Val Val Leu
         -15                    -10                     -5

Xaa Leu Phe Asn Arg Cys Ala Leu Phe Xaa Ser Tyr Pro Lys Trp Asp
 1               5                   10                     15

Xaa Cys Pro Gly Asn Tyr Thr Asn Pro
                 20
```

(2) INFORMATION FOR SEQ ID NO: 434:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -16..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7.5
                        seq GCMLLFVFGFVGG/AV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```
Met Ser Pro Gly Cys Met Leu Leu Phe Val Phe Gly Phe Val Gly Gly
         -15                    -10                     -5

Ala Val Val Ile Asn Ser Ala Ile Leu Val Ser Leu Ser Val Leu Leu
 1               5                   10                     15

Leu Val His Phe Ser Ile Ser Thr Gly Val Pro Ala Leu Thr Gln Asn
                 20                  25                     30

Leu Pro Arg Ile Leu Arg Lys Glu Arg Pro Gly
         35                  40
```

(2) INFORMATION FOR SEQ ID NO: 435:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 67 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens

           (F) TISSUE TYPE: Brain

     (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -15..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION: score 7.5
                                    seq LLLGIALLAYVAS/VW

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val
-15   -10   -5   1

Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu
               5   10   15

Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys
        20   25   30

Ile Arg Asp Leu Xaa Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys
    35   40   45

Phe Leu Ser
 50

(2) INFORMATION FOR SEQ ID NO: 436:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 151 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -23..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION: score 7.5
                                    seq LVLLLTLPLHLMA/LL

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu Thr
        -20   -15   -10

Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys
    -5   1   5

Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro Lys Ser Asn
 10   15   20   25

Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly
            30   35   40

Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu Glu Leu Gly Cys Gly
            45   50   55

Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
            60   65   70

Leu Asp Pro Asn Pro His Phe Glu Lys Phe Leu Thr Lys Ser Met Ala
        75   80   85

Glu Asn Arg His Leu Gln Tyr Glu Arg Phe Val Val Ala Pro Gly Glu
    90   95   100   105

Asp Met Arg Xaa Leu Ala Asp Gly Ser Met Asp Val Val Val Cys Thr
                110   115   120

Leu Val Leu Cys Ser Val Gln
                125

(2) INFORMATION FOR SEQ ID NO: 437:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 103 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -35..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 7.4
                            seq SLLLSLELASGSG/QG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Glu Ala Ala Ser Pro Ser Asn Ser Thr Gly Val Glu Arg Xaa Ala
-35   -30   -25   -20

Asp Leu Met Asp Ala Asp Ser Leu Leu Leu Ser Leu Glu Leu Ala Ser
            -15   -10   -5

Gly Ser Gly Gln Gly Leu Ser Pro Asp Arg Arg Ala Ser Leu Leu Thr
            1   5   10

Ser Leu Met Leu Val Lys Arg Asp Tyr Arg Tyr Asp Arg Val Leu Phe
    15   20   25

Trp Gly Arg Ile Leu Gly Leu Val Ala Asp Tyr Tyr Ile Ala Gln Gly
    30   35   40   45

```
Leu Ser Glu Asp Gln Leu Ala Pro Arg Lys Thr Leu Tyr Arg Ser Arg
              50                  55                  60

Ser Arg Lys Arg Pro Ala Leu
              65 *
```

(2) INFORMATION FOR SEQ ID NO: 438:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 70 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -43..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 7.4
                                   seq VLVKLLSSSASTS/RP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

```
Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Ala Val Arg Pro
        -40                  -35                  -30

Ala Leu Pro Ser Ser Lys Pro Cys Leu Leu Thr Ser Pro Ala Val Leu
        -25                  -20                  -15

Val Lys Leu Leu Ser Ser Ser Ala Ser Thr Ser Arg Pro Pro Asp Leu
        -10                  -5                    1                  5

Gly His Leu Trp Gln Pro Ser Ser Ser Val Pro Leu His Arg Pro Pro
                 10                  15                  20

His Thr Ala Pro Pro Ala
                 25
```

(2) INFORMATION FOR SEQ ID NO: 439:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

```
      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -41..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION:  score 7.4
                               seq ILPLLFGCLGVFG/LF

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:
```

```
Met Lys Leu Ile Asp Tyr Gly Leu Ser Gly Tyr Gln Glu Glu Ser Ala
    -40               -35             -30

Glu Val Lys Ala Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu
-25               -20             -15                     -10

Leu Phe Gly Cys Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp
             -5             1                 5

Val Arg Gly Lys Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly
         10             15             20

Ala Thr Ser Gly Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Xaa
     25             30             35

Gly Ala Lys Leu Val Leu Cys Glu Xaa Glu Trp Trp Gly Leu Glu Glu
 40             45             50                     55

Leu Ile Arg Glu Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His
             60             65             70

Lys
```

```
(2) INFORMATION FOR SEQ ID NO: 440:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 44 amino acids
           (B) TYPE: AMINO ACID
           (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Brain

      (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: -19..-1
           (C) IDENTIFICATION METHOD: Von Heijne matrix
           (D) OTHER INFORMATION:  score 7.4
                               seq PMLLRALAQAARA/GP

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:
```

```
Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
         -15             -10                     -5
```

Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
          1   5   10

Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Gln
     15   20   25

(2) INFORMATION FOR SEQ ID NO: 441:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 84 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -67..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 7
                                     seq IWTLLSSVIRCLC/AI

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser
       -65   -60   -55

Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe
   -50   -45   -40

Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu
-35   -30   -25   -20

Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg
             -15   -10   -5

Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr
          1   5   10

Leu Trp Thr Phe
     15

(2) INFORMATION FOR SEQ ID NO: 442:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 29 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:

```
            (A)  ORGANISM: Homo Sapiens
            (F)  TISSUE TYPE: Brain

        (ix) FEATURE:
            (A)  NAME/KEY: sig_peptide
            (B)  LOCATION: -14..-1
            (C)  IDENTIFICATION METHOD: Von Heijne matrix
            (D)  OTHER INFORMATION:  score 6.8
                                    seq IFLTLSLDSRVSA/IR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:


Met Ile Phe Leu Thr Leu Ser Leu Asp Ser Arg Val Ser Ala Ile Arg
              -10                   -5                   1

Ser Pro Asn Phe Val Tyr Arg Ser Pro Thr Xaa His Gly
         5                   10               15




(2) INFORMATION FOR SEQ ID NO: 443:

        (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 101 amino acids
            (B)  TYPE: AMINO ACID
            (D)  TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A)  ORGANISM: Homo Sapiens
            (F)  TISSUE TYPE: Brain

        (ix) FEATURE:
            (A)  NAME/KEY: sig_peptide
            (B)  LOCATION: -29..-1
            (C)  IDENTIFICATION METHOD: Von Heijne matrix
            (D)  OTHER INFORMATION:  score 6.8
                                    seq LIFLCGAALLXVG/IW

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:


Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
              -25                   -20                  -15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Xaa Val Gly Ile Trp Val
              -10                   -5                   1

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
         5                   10               15

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
    20                   25                   30               35

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Xaa Ala Lys Thr
              40                   45                   50

Glu Ser Xaa Cys Ala Leu Val Thr Phe Phe Xaa Ile Leu Leu Leu Ile
              55                   60                   65
```

Phe Ile Ala Asp Val
      70

(2) INFORMATION FOR SEQ ID NO: 444:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 97 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -35..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 6.4
                                     seq SACLLLCPTWTNP/QL

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Ala Glu Ala Ala Leu Glu Ala Val Arg Xaa Ser Tyr Glu Asn Ser
-35   -30   -25   -20

Arg Pro Leu Gln Gly Ser Ser Ala Cys Leu Leu Leu Cys Pro Thr Trp
            -15   -10   -5

Thr Asn Pro Gln Leu Arg Ser Thr Ser Thr Gly Thr Gly Ser Ala Pro
             1   5   10

Thr Gly Arg Ala Leu Ser Ala Thr Leu Cys Ser Thr Gly Arg Pro Ser
     15   20   25

Xaa Xaa Trp Ser Leu Pro Tyr Phe Arg Ala Thr Val Gly Ser Thr Glu
 30   35   40   45

Val Ser Val Ala Val Thr Pro Asp Gly Tyr Ala Asp Ala Val Arg Xaa
             50   55   60

Asp

(2) INFORMATION FOR SEQ ID NO: 445:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 34 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:

              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -19..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 6.4
                                       seq SVFLLMVNGQVES/AQ

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
              -15   -10   -5

Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys Lys Tyr
              1   5   10

Cys Gln
    15

(2) INFORMATION FOR SEQ ID NO: 446:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 36 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -28..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 6
                                       seq IGLMFLMLGCALP/IY

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
              -25   -20   -15

Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
         -10   -5   1

Tyr Trp Pro Trp
  5

(2) INFORMATION FOR SEQ ID NO: 447:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 39 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -17..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.9
                                    seq ILLFGTLLMNAGA/VL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
     -15   -10   -5

Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln Gly Phe Gly
     1   5   10   Gly   15

Glu Glu Ser Arg Glu Pro Trp
            20

(2) INFORMATION FOR SEQ ID NO: 448:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 28 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -16..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.9
                                    seq MILTLSLFGSCIS/NF

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Lys Thr Met Ile Leu Thr Leu Ser Leu Phe Gly Ser Cys Ile Ser
    -15   -10   -5

Asn Phe Glu Arg Tyr Met Thr Glu Arg Ser Ile Gln
    1   5   10

(2) INFORMATION FOR SEQ ID NO: 449:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 82 amino acids
        (3) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -39..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.9
                              seq SVSVLSSLGIVLA/VV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Asp Trp Arg Val Pro Pro Ser Xaa Xaa Asp Pro Gly His Gln Asp
           -35   -30   -25

Ile Pro Leu Pro Val Thr Xaa Xaa Phe Ile Ser Val Ser Val Leu Ser
           -20   -15   .   . .   -10

Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr
        -5   .   1   5

Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn
 10   15   20   25

Leu Thr Ala Val Gly Cys Ser Xaa Ala Leu Ala Ala Val Phe Pro Trp
           30   35   40

Gly Ser

(2) INFORMATION FOR SEQ ID NO: 450:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -16..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 5.8

                          seq AALPAWLSLQSRA/RT

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser Arg Ala
   -15   -10   -5

Arg Thr Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr Pro Val
  1   5   10   15

Pro Xaa Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro
           20   25   30

Arg Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Asp Gln
          35   40   45

Asp Trp Pro Xaa Val Tyr Pro Val Ala Ala Pro Phe Lys Pro Ser Ala
   50   55   60

Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro
  65   70   75   80

Trp Xaa Arg Arg Glu Ser Xaa Thr Phe Lys Asp Ser Asn Phe Leu His
           85   90   95

Leu

(2) INFORMATION FOR SEQ ID NO: 451:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 29 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -25..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.8
                                    seq LWISACAMLLCHG/SL

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Ala Met Val Ser Ala Met Ser Trp Val Leu Tyr Leu Trp Ile Ser
-25   -20   -15   -10

Ala Cys Ala Met Leu Leu Cys His Gly Ser Leu Gln Arg
                 -5   1

(2) INFORMATION FOR SEQ ID NO: 452:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 78 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -69..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 5.7
                                 seq LCRLLCLVRLFCC/SS

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
            -65   -60   -55

Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val
            -50   -45   -40

Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe
            -35   -30   -25

Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val
            -20   -15   -10

Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Gly
 -5   1   5

(2) INFORMATION FOR SEQ ID NO: 453:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 65 amino acids
             (B) TYPE: AMINO ACID
             (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Homo Sapiens
             (F) TISSUE TYPE: Brain

       (ix) FEATURE:
             (A) NAME/KEY: sig_peptide
             (B) LOCATION: -21..-1
             (C) IDENTIFICATION METHOD: Von Heijne matrix
             (D) OTHER INFORMATION: score 5.6
                                 seq LVLSLQFLLLSYD/LF

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
    -20   -15   -10

Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 -5   1   5   10

Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
            15   20   25

Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser
         30   35   40

Arg

(2) INFORMATION FOR SEQ ID NO: 454:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 27 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -24..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.5
                                    seq MGVCLLIPGLATA/CI

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Trp Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu
            -20   -15   -10

Leu Ile Pro Gly Leu Ala Thr Ala Cys Ile Arg
            -5   1

(2) INFORMATION FOR SEQ ID NO: 455:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 46 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -22..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION: score 5.5
                              seq LADPLXLFPFSEG/LP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Arg Pro Ser Pro Leu Ser Gly Ile Leu Ala Asp Pro Leu Xaa Leu
        -20   -15   -10

Phe Pro Phe Ser Glu Gly Leu Pro Arg Arg Arg Ala Ala Ser Arg Ser
     -5   1   5   10

Arg Leu Gln Thr Pro Ser Ala Arg Cys Ser Pro Arg Pro Gly
                15   20

(2) INFORMATION FOR SEQ ID NO: 456:

    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 30 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

    (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -27..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 5.4
                                  seq SLMMAQXFIPAVA/KV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Arg Glu Ser Leu Ser Xaa Arg Ser Trp His Leu Pro Ala Ser Leu
        -25   -20   -15

Met Met Ala Gln Xaa Phe Ile Pro Ala Val Ala Lys Val Gly
    -10   -5   1

(2) INFORMATION FOR SEQ ID NO: 457:

    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 60 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

```
    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: -58..-1
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 5.4
                                 seq LSLHLLATRACYG/IL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:


Met Ser Gly Val Val Pro Thr Ala Pro Glu Gln Pro Ala Xaa Glu Met
        -55                 -50             -45

Glu Asn Gln Thr Lys Pro Pro Asp Pro Arg Pro Asp Ala Pro Pro Glu
        -40                 -35             -30

Tyr Ser Ser His Xaa Phe Thr Arg Thr Pro Trp Lys Gln Leu Ser Leu
    -25                 -20                 -15

His Leu Leu Ala Thr Arg Ala Cys Tyr Gly Ile Leu
-10                 -5                  1




(2) INFORMATION FOR SEQ ID NO: 458:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 83 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

       (ii) MOLECULE TYPE: PROTEIN

       (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

       (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -77..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.3
                                    seq TWVFTCLVFFCFG/LS

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:


Met Trp Arg Tyr Gln Phe Gly Trp Gly Val Ile Thr Arg Gly Pro Arg
        -75                 -70                 -65

Glu Ile Pro Phe Pro Pro Ser Leu Leu Ala Ser Glu Ser Leu Leu Pro
    -60                 -55                 -50

Pro Leu Pro Asp Leu Val Leu Thr Cys Thr Ser Leu Gly Phe Val Thr
-45                 -40                 -35                 -30
```

Arg Val Trp. Met Ser Leu Asn Leu Asn Glu Leu Ser Leu Tyr Ser Arg
              -25   -20   -15

Thr Trp Val Phe Thr Cys Leu Val Phe Phe Cys Phe Gly Leu Ser Xaa
          -10   -5   1

Ser Leu Gly
    5

(2) INFORMATION FOR SEQ ID NO: 459:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -29..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.2
                                    seq FFMLLGSLLPVKI/IE

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Val Lys Leu Leu Val Ala Lys Ile Leu Cys Met Val Gly Val Phe
              -25   -20   -15

Phe Phe Met Leu Leu Gly Ser Leu Leu Pro Val Lys Ile Ile Glu Thr
          -10   -5   1

Asp Phe Glu Lys Ala Pro Gly
    5   10

(2) INFORMATION FOR SEQ ID NO: 460:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -17..-1

```
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 5.2
                                  seq IMCLIGLKANASS/ET

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:


Met Pro Val Ser Ile Met Cys Leu Ile Gly Leu Lys Ala Asn Ala Ser
     -15                 -10                 -5

Ser Glu Thr His Ser Gly
     1           5




(2) INFORMATION FOR SEQ ID NO: 461:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 26 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -17..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 5.2
                                  seq LLYLVLEKLVSRA/FQ

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:


Met Lys Val Ile Leu Leu Tyr Leu Val Leu Glu Lys Leu Val Ser Arg
     -15                 -10                 -5

Ala Phe Gln Asn Val Glu Ala Pro His Gly
     1           5




(2) INFORMATION FOR SEQ ID NO: 462:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 46 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
```

(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
                        seq LLLGGRVCXPSLA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ala Val Thr Leu Ser Leu Leu Leu Gly Gly Arg Val Cys Xaa Pro
            -15   -10   -5

Ser Leu Ala Val Gly Ser Arg Pro Gly Gly Trp Arg Ala Gln Ala Leu
            1   5   10

Leu Ala Gly Ser Arg Thr Pro Ile Pro Thr Gly Asn Arg Arg
    15   20   25

(2) INFORMATION FOR SEQ ID NO: 463:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 49 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -23..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 5.1
                        seq LLPELGVVTPAQG/PR

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Leu Asn Gln Thr Ser Gly Arg Thr Ser Leu Leu Pro Glu Leu Gly
            -20   -15   -10

Val Val Thr Pro Ala Gln Gly Pro Arg Arg Arg Val Trp Cys Gly His
            -5   1   5

Ser Lys Ala Lys Ala Arg Lys Ser Tyr Cys Ala Arg Ala Ile Asp Cys
    10   15   20   25

Gln

(2) INFORMATION FOR SEQ ID NO: 464:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 135 amino acids
            (B) TYPE: AMINO ACID
            (C) TOPOLOGY: LINEAR

```
(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Homo Sapiens
     (F) TISSUE TYPE: Brain

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: -79..-1
     (C) IDENTIFICATION METHOD: Von Heijne matrix.
     (D) OTHER INFORMATION:  score 5
                             seq SFLGFSAPTPIQA/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:
```

```
Met Thr Ser Glu Asn Leu Val Gln Thr Ala Pro Lys Lys Lys Lys Asn
            -75                 -70             -65

Lys Gly Lys Lys Gly Leu Glu Pro Ser Gln Ser Thr Ala Ala Lys Val
        -60             -55             -50

Pro Lys Lys Ala Lys Thr Trp Ile Pro Glu Val His Asp Gln Lys Ala
    -45                 -40             -35

Asp Val Ser Ala Trp Lys Asp Leu Phe Val Pro Arg Pro Val Leu Arg
    -30             -25             -20

Ala Leu Ser Phe Leu Gly Phe Ser Ala Pro Thr Pro Ile Gln Ala Leu
-15             -10             -5                      1

Thr Leu Ala Pro Ala Ile Arg Asp Lys Leu Asp Ile Leu Gly Ala Ala
            5                 10              15

Glu Thr Gly Ser Gly Lys Thr Leu Ala Phe Ala Ile Pro Met Ile His
        20              25              30

Ala Val Leu Gln Trp Gln Lys Arg Asn Ala Ala Pro Pro Pro Ser Asn
    35              40              45

Thr Glu Ala Pro Pro Gly Glu
50              55
```

```
(2) INFORMATION FOR SEQ ID NO: 465:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 79 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
```

(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
                       seq WHXLIPLTWACMA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Ala Ala Phe Gly Arg Gln Xaa Xaa Xaa Trp His Xaa Leu Ile Pro
          -20   -15   Trp His -10

Leu Thr Trp Ala Cys Met Ala Arg Gln Thr Pro His Leu Gly Glu Gln
     -5   1   5

Arg Arg Thr Thr Ala Ser Leu Xaa Arg Lys Leu Thr Thr Ala Ser Asn
 10   15   20   25

Gly Gly Val Ile Glu Glu Leu Ser Cys Val Arg Ser Asn Asn Tyr Val
             30   35   40

Gln Glu Pro Glu Cys Arg Arg Asn Leu Val Gln Cys Leu Leu Trp
         45   50   55

(2) INFORMATION FOR SEQ ID NO: 466:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 68 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -57..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.9
                                   seq GWFLSGCPHGSSA/TW

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ser Leu Thr Ser Ser Pro Lys Lys Arg Arg Ser Ile Cys Phe Asp
    -55   -50   -45

Arg Phe Leu Met Pro Gln Ser Gln Ser Gly Pro Ser Ser Leu Gly Glu
    -40   -35   -30

Ser Tyr Arg Thr Gly Val Gly Phe Leu Ile Pro Glu Gly Trp Phe Leu
-25   -20   -15   -10

Ser Gly Cys Pro His Gly Ser Ser Ala Thr Trp Thr Lys Cys Gln Thr
             -5   1   5

Ser Ala Ser Leu

10

(2) INFORMATION FOR SEQ ID NO: 467:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -39..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.8
                          seq SLXFCLSPPPSPS/LR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Gly Glu Leu Gly Asn Arg Ser Arg Cys Ile Leu Phe Leu Ser Glu
          -35   -30   -25

Asn Pro Cys Leu Ser Glu Ser Ile Phe Gln Ser Leu Xaa Phe Cys Leu
          -20   -15   -10

Ser Pro Pro Pro Ser Pro Ser Leu Arg Pro Ser Pro Ser Arg
       -5   1   5

(2) INFORMATION FOR SEQ ID NO: 468:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 111 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -93..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.7
                          seq VLLLRQXFAQAEK/WY

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
Met Ala Glu Leu Gly Leu Asn Glu His His Gln Asn Glu Val Ile Asn
        -90                 -85                 -80

Tyr Met Arg Phe Ala Arg Ser Lys Arg Gly Leu Arg Leu Lys Thr Val
        -75                 -70                 -65

Asp Ser Cys Phe Gln Asp Leu Lys Glu Ser Arg Leu Val Glu Asp Thr
    -60                 -55                 -50

Phe Thr Ile Asp Glu Val Ser Glu Val Leu Asn Gly Leu Gln Ala Val
-45                 -40                 -35                 -30

Val His Ser Glu Val Glu Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn
            -25                 -20                 -15

Val Leu Leu Leu Arg Gln Xaa Phe Ala Gln Ala Glu Lys Trp Tyr Leu
        -10                 -5                  1

Lys Leu Gln Thr Asp Ile Ser Glu Leu Glu Asn Arg Glu Leu Leu
    5               10                  15
```

(2) INFORMATION FOR SEQ ID NO: 469:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 70 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -49..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.6
                               seq SWAVGLLYAVAQG/SK

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```
Met Val Thr Leu Pro Ser Gly Thr Trp Ala Phe Ser Cys Pro Tyr Leu
        -45                 -40                 -35

Ala Leu Val Asp Gly Gly Met Leu Gly Ser Ala Arg Glu Asp Ala His
        -30                 -25                 -20

Ala Ser Val Val Ser Trp Ala Val Gly Leu Leu Tyr Ala Val Ala Gln
        -15                 -10                 -5

Gly Ser Lys Arg Arg Lys Val Gln Asp Val Lys Pro Leu Xaa Trp Ser
    1               5                   10                  15

Arg Thr Gly Thr Leu Gly
        20
```

(2) INFORMATION FOR SEQ ID NO: 470:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 80 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -68..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.6
                          seq LPFSLVSMLVTQG/LV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
        -65   -60   -55

Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Xaa Xaa Leu
       -50   -45   -40

His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
    -35   -30   -25

Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20   -15   -10   -5

Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
            1   5   10

(2) INFORMATION FOR SEQ ID NO: 471:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 71 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -69..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.5
                          seq FILSLCVLCIVLT/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Leu Leu Met Lys Ser Ile Leu Leu Lys Val Val Cys Val Leu Cys
          -65   -60   -55

Ile Tyr Leu Lys Phe Lys Leu Met Ala Leu Ile Tyr Val Pro Asp Lys
          -50   -45   -40

Asn Asn Thr Asn Asn Asn Ile Leu Arg Tyr Asn His Asn Glu Ile Ser
          -35   -30   -25

Ile Gly Ile Ser Val Gln Cys His Phe Ile Leu Ser Leu Cys Val Leu
  -20   -15   -10

Cys Ile Val Leu Thr Thr Gly
-5   1

(2) INFORMATION FOR SEQ ID NO: 472:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 50 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

      (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -16..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 4.5
                                    seq RLLLRRFLASVIS/RK

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser
  -15   -10   -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
  1   5   10   15

Gln Thr Pro Xaa Cys Ser Xaa Gly Gly Leu Thr Val Thr Pro Asn Pro
          20   25   30

Ser Arg

(2) INFORMATION FOR SEQ ID NO: 473:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 103 amino acids

```
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: PROTEIN

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -77..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.4
                          seq FEARIALLPLLQA/ET

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:
```

Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Xaa Gly Gly Tyr
        -75   -70   -65

Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
    -60   -55   -50

Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
-45   -40   -35   -30

Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Leu Gln Ile Glu Asp
            -25   -20   -15

Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
            -10   -5   1

Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
    5   10   15

Ile Met Lys Asp Val Pro Gly
20   25

```
(2) INFORMATION FOR SEQ ID NO: 474:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 77 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: PROTEIN

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -54..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.3
                          seq LLSLAILSHISTP/GC
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:


```
Met Arg His Leu Val Thr Glu Glu Leu Phe Pro Cys Ser Asn Leu Glu
              -50               -45             -40

Asp Val Val Glu Asp Asn Ser His Ser Tyr Phe Thr Leu Arg Ile Thr
              -35               -30             -25

Met Ala Cys Lys Gly Val Pro Ser Thr Leu Leu Ser Leu Ala Ile Leu
              -20               -15             -10

Ser His Ile Ser Thr Pro Gly Cys Glu Trp His Val Ile Tyr Val Ser
      -5               1               5                  10

Ser Xaa Gly Leu Tyr Leu Val Val Glu Met Thr Asp Arg
              15               20
```


(2) INFORMATION FOR SEQ ID NO: 475:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 80 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -76..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.3
                                    seq FRLLXVFAYGTYA/DY

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:


```
Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
    -75               -70             -65

Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
-60               -55               -50             -45

Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
              -40               -35             -30

Met Pro Asn Val Arg Glu Leu Ala Glu Ser Xaa Phe Ala Ser Thr Phe
              -25               -20             -15

Arg Leu Leu Xaa Val Phe Ala Tyr Gly Thr Tyr Ala Asp Tyr Xaa Ala
          -10               -5               1
```

(2) INFORMATION FOR SEQ ID NO: 476:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -34..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.3
                         seq QLFAFLNLLPVEA/DI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Xaa
        -30   -25   -20

Thr Ile Leu Xaa Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
        -15   -10   -5

Glu Ala Asp Ile Xaa Ala Tyr Asn Phe Glu Asn Ala Ser
     1   5   10

(2) INFORMATION FOR SEQ ID NO: 477:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -16..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 4.2
                         seq EVVSLSYCGVSWG/RI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

Met Gly Trp Glu Val Val Ser Leu Ser Tyr Cys Gly Val Ser Trp Gly
        -15   -10   -5

Arg Ile Ser Pro Asn Leu Asn Lys Pro Val Asn Arg

1   5   10

(2) INFORMATION FOR SEQ ID NO: 478:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 72 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -32..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.2
                                     seq CWELFCLEHGIQA/DG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln Ile
        -30   -25   -20

Gly Asn Ala Cys Trp Glu Leu Phe Cys Leu Glu His Gly Ile Gln Ala
    -15   -10   -5

Asp Gly Thr Phe Asp Ala Gln Ala Ser Lys Ile Asn Asp Asp Asp Ser
 1   5   10   15

Phe Thr Thr Phe Phe Ser Glu Thr Gly Thr Ser Leu Leu Met Glu Arg
            20   25   30

Leu Xaa Leu Asp Tyr Gly Lys Lys
        35   40

(2) INFORMATION FOR SEQ ID NO: 479:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 46 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -25..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix

       (D) OTHER INFORMATION: score 4.2
                      seq LDLLRGLPRVSLA/NL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu
-25   -20   -15   -10

Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly
                -5   1   5

Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Trp
        10   15   20

(2) INFORMATION FOR SEQ ID NO: 480:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 68 amino acids
       (B) TYPE: AMINO ACID
       (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN ·

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Homo Sapiens
       (F) TISSUE TYPE: Brain

    (ix) FEATURE:
       (A) NAME/KEY: sig_peptide
       (B) LOCATION: -25..-1
       (C) IDENTIFICATION METHOD: Von Heijne matrix
       (D) OTHER INFORMATION: score 4.2
                      seq MFAASXLAMCAGA/EV

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25   -20   -15   -10

Ser Xaa Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
                -5   1   5

Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
        10   15   20

Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
        25   30   35

Ser Gln Gln Glu
40

(2) INFORMATION FOR SEQ ID NO: 481:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 32 amino acids

```
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -24..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.2
                                    seq SLPALALSLRASP/RX

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:
```

```
Met Ala Val Gln Cys Val Arg Leu Ala Arg Arg Ser Leu Pro Ala Leu
            -20                 -15                 -10

Ala Leu Ser Leu Arg Ala Ser Pro Arg Xaa Leu Cys Thr Ala Thr Lys
            -5                   1                   5

Gln Lys Asn Ser Gly Gln Asn Leu Glu Glu Asp Met Gly Gln Ser Glu
     10                  15                  20

Gln Lys Ala Asp Pro Pro Ala Thr Glu Lys Thr Leu Leu Glu Glu Lys
 25                  30                  35                  40

Val Lys Leu Glu Glu Gln Leu Lys Glu Thr Val Glu Lys Tyr Lys Arg
                45                  50                  55

Ala Arg
```

```
(2) INFORMATION FOR SEQ ID NO: 482:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 42 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: PROTEIN

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -37..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 4.2
                                    seq RLMHHYLSTPTSA/RP

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:
```

Met Phe Ser Ile Ile Ser Arg Ser Arg Ala Cys Ser Met Tyr Phe Lys
    -35   -30   -25

Glu Asn Ala Lys Pro Ser Gln Leu Arg Leu Met His His Tyr Leu Ser
    -20   -15   -10

Thr Pro Thr Ser Ala Arg Pro His His Leu
 -5   1   5

(2) INFORMATION FOR SEQ ID NO: 483:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 35 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -16..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 4.1
                                    seq LLPATSLAGPVLS/TL

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
    -15   -10   -5

Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp
 1   5   10   15

Asp Pro Gly

(2) INFORMATION FOR SEQ ID NO: 484:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 98 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -70..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix

          (D) OTHER INFORMATION: score 4
                                  seq IAVLYLHLYDVFG/DP

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Leu Ile Ile Thr Asn Pro Trp Pro Lys Tyr Phe Asp Ala Ala Gly
-70   -65   -60   -55

Arg Leu Thr Pro Glu Phe Ser Gln Arg Leu Thr Asn Lys Ile Arg Glu
              -50   -45   -40

Leu Leu Gln Gln Met Glu Arg Gly Leu Lys Ser Ala Asp Xaa Xaa Asp
          -35   -30   -25

Gly Thr Gly Tyr Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His
          -20   -15   -10

Leu Tyr Asp Val Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly
     -5   1   5   10

Tyr Val Lys Gln Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe
              15   20   25

Gln Gly

(2) INFORMATION FOR SEQ ID NO: 485:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 47 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

     (ii) MOLECULE TYPE: PROTEIN

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -21..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION: score 3.9
                                  seq AWLAQGSSSAGWG/LE

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Cys Ala Thr Glu Thr Val Arg Ala Trp Leu Ala Gln Gly Ser Ser
    -20   -15   -10

Ser Ala Gly Trp Gly Leu Glu Arg Lys Gln Gly Val Ser Ala His Arg
 -5   1   5   10

Met Pro Ala Leu Arg Trp Leu Gln Lys Ser Val Pro Gly Xaa Met
              15   20   25

(2) INFORMATION FOR SEQ ID NO: 486:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -46..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                           seq AAAFCLKXXGANT/HP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met Leu Leu Leu Ala Thr His Pro Glu Thr Val Gly Gln Val Thr Leu
   -45   -40   -35

Arg Val Xaa Pro Val Ser Leu Glu Val Ser Ile Gln Met Cys Ala Ala
-30   -25   -20   -15

Ala Ala Ala Ala Phe Cys Leu Lys Xaa Xaa Gly Ala Asn Thr His Pro
          -10   -5   1

(2) INFORMATION FOR SEQ ID NO: 487:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 86 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -64..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                           seq GLGGAQLQGGAXG/RG

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Met Ala Ala Ser Ser Ala Thr Pro Ala Pro Xaa Xaa Ser Gln Arg Cys
       -60   -55   -50

```
Gly Ala Asp Ala Gly Ser Ala Ala Arg Ile Val Phe Arg Trp Gly Arg
        -45             -40             -35

Gly Arg Arg Gly Ala Arg Ser Pro Glu Gly Ser Gly His His Gly Arg
        -30             -25             -20

Ala Asn Ser Gly Leu Gly Gly Ala Gln Leu Gln Gly Gly Ala Xaa Gly
    -15             -10             -5

Arg Gly Ser Met Ala Pro Leu Arg Ala Ser Ala Gly Gln Thr Arg Asp
 1           5               10              15

Gly Pro Thr Gln Pro Gly
            20
```

(2) INFORMATION FOR SEQ ID NO: 488:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -17..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.9
                            seq PLAGLAAAALGRA/PP

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```
Met Leu Arg Arg Pro Leu Ala Gly Leu Ala Ala Ala Ala Leu Gly Arg
        -15             -10             -5

Ala Pro Pro Asp Gly Leu Leu Cys Ser Leu Pro Gly Val Ala Val Glu
 1           5               10              15

Asp Pro Val Gln Asp Ser Ala Gly Phe Ser Phe Ser Leu Met Asp Arg
            20              25              30

Pro Lys
```

(2) INFORMATION FOR SEQ ID NO: 489:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 53 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

```
    (vi) ORIGINAL SOURCE:
         (A) ORGANISM: Homo Sapiens
         (F) TISSUE TYPE: Brain

    (ix) FEATURE:
         (A) NAME/KEY: sig_peptide
         (B) LOCATION: -17..-1
         (C) IDENTIFICATION METHOD: Von Heijne matrix
         (D) OTHER INFORMATION:  score 3.8
                                 seq GFVAALVAGGVAG/VS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:
```

```
Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
        -15               -10               -5

Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1             5               10                  15

Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
              20                  25                  30

Ile Tyr Ala Ser Trp
              35
```

```
(2) INFORMATION FOR SEQ ID NO: 490:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: PROTEIN

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -21..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 3.8
                                seq SMDLLTLLFQRRS/HQ

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:
```

```
Met Ile Val Trp Phe Glu Gly Ile Ser Met Asp Leu Leu Thr Leu Leu
    -20             -15               -10

Phe Gln Arg Arg Ser His Gln Val Thr Gln Leu Leu Val Ser Ser Thr
 -5             1               5                   10

Gly Asn Trp Leu Arg Gln Tyr Leu Cys Ala Ser Leu Thr Ile Ala Gly
              15                  20                  25
```

Arg Arg

(2) INFORMATION FOR SEQ ID NO: 491:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 50 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -20..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.8
                                     seq ALDALMFPARRRA/AV

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Arg Thr Phe Val His Phe Ala Leu Asp Ala Leu Met Phe Pro Ala
-20   -15   -10   -5

Arg Arg Arg Ala Ala Val Thr Arg Leu Ser Glu Arg Leu Ser Leu Cys
                 1   5   10

Phe Cys Leu His Ser Arg Leu Gln Asp Pro Ala Ala Arg Pro Arg Pro
            15   20   25

Ser Trp
    30

(2) INFORMATION FOR SEQ ID NO: 492:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 99 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -61..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.8
                                     seq LVMTFLFRNGSLQ/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Ala Ala Pro Pro Gln Leu Arg Ala Leu Leu Val Val Val Asn Ala
-60   .   -55   -50

Leu Leu Arg Lys Arg Arg Tyr His Ala Ala Leu Ala Val Leu Lys Gly
-45   -40   -35   -30

Phe Arg Asn Gly Ala Val Tyr Gly Ala Lys Ile Arg Ala Pro His Ala
             -25   -20   -15

Leu Val Met Thr Phe Leu Phe Arg Asn Gly Ser Leu Gln Glu Lys Leu
             -10   -5   1

Trp Ala Ile Leu Gln Ala Thr Tyr Ile His Ser Trp Asn Leu Ala Arg
   5   10   15

Phe Val Phe Thr Tyr Lys Gly Leu Arg Ala Leu Gln Ser Tyr Ile Gln
20   25   30   35

Gly Pro Gly

(2) INFORMATION FOR SEQ ID NO: 493:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 79 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -18..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.8
                                    seq GXALGLLPSLAKA/ED

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Pro Val Asp Leu Gly Xaa Ala Leu Gly Leu Leu Pro Ser Leu Ala
             -15   -10   -5

Lys Ala Glu Asp Ser Gln Phe Ser Glu Ser Asp Ala Ala Leu Gln Glu
         1   5   10

Glu Leu Ser Ser Pro Glu Thr Ala Arg Gln Leu Phe Arg Gln Phe Arg
15   20   25   30

Tyr Gln Val Met Ser Gly Pro His Glu Thr Leu Lys Xaa Leu Arg Lys
   .   35   40   45

Leu Cys Phe Gln Trp Leu Gln Pro Glu Val His Thr Lys Glu Gly

                50   55   60

(2) INFORMATION FOR SEQ ID NO: 494:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 139 amino acids
              (B) TYPE: AMINO ACID
              (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Homo Sapiens
              (F) TISSUE TYPE: Brain

        (ix) FEATURE:
              (A) NAME/KEY: sig_peptide
              (B) LOCATION: -72..-1
              (C) IDENTIFICATION METHOD: Von Heijne matrix
              (D) OTHER INFORMATION: score 3.8
                                       seq LMGLALAVYKCQS/MG

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
        -70   -65   -60

Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
        -55   -50   -45

Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
-40   -35   -30   -25

Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
                -20   -15   -10

Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
                -5   1   5

Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Ser Val
        10   15   20

Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala Pro Gly Pro Tyr
25   30   35   40

Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro Val Ala Pro Gln
                45   50   55

His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys
                60   65

(2) INFORMATION FOR SEQ ID NO: 495:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 102 amino acids
              (B) TYPE: AMINO ACID

```
        (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

(ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -51..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 3.8
                                seq NVLFVAGLAFVIG/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:
```

```
Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
    -50              -45              -40

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
-35              -30              -25                      -20

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
                -15              -10                      -5

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
                 1               5                       10

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
    15              20               25

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
    30              35               40                      45

Leu Phe Arg Gly Leu Gly
                50
```

```
(2) INFORMATION FOR SEQ ID NO: 496:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 53 amino acids
                (B) TYPE: AMINO ACID
                (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
                (A) ORGANISM: Homo Sapiens
                (F) TISSUE TYPE: Brain

        (ix) FEATURE:
                (A) NAME/KEY: sig_peptide
                (B) LOCATION: -33..-1
                (C) IDENTIFICATION METHOD: Von Heijne matrix
                (D) OTHER INFORMATION:  score 3.6
                                        seq LAVFQMLKSMCAG/QR
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ala Ala Ser Gly Ala Pro Arg Ile Leu Val Asp Leu Leu Lys Leu
          -30   -25   -20

Xaa Val Ala Pro Leu Ala Val Phe Gln Met Leu Lys Ser Met Cys Ala
          -15   -10   -5

Gly Gln Arg Leu Ala Ser Glu Pro Gln Asp Pro Ala Ala Val Ser Leu
    1   5   10   15

Pro Thr Ser Ser Gly
              20

(2) INFORMATION FOR SEQ ID NO: 497:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 92 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -26..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 3.6
                                    seq ARSLLQFLRLVGQ/LK

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Ala Ser Val Ser Ser Ala Thr Phe Ser Gly His Gly Ala Arg Ser
    -25   -20   -15

Leu Leu Gln Phe Leu Arg Leu Val Gly Gln Leu Lys Arg Val Pro Arg
-10   -5   1   5

Thr Gly Trp Val Tyr Arg Asn Val Gln Arg Pro Glu Ser Val Ser Asp
          10   15   20

His Met Tyr Arg Met Ala Val Met Ala Met Val Ile Lys Asp Asp Arg
          25   30   35

Leu Asn Lys Asp Arg Cys Val Arg Leu Ala Leu Val His Asp Met Ala
    40   45   50

Glu Cys Ile Val Gly Asp Ile Ala Pro Ala Asp Gly
55   60   65

(2) INFORMATION FOR SEQ ID NO: 498:

```
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

    (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -16..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 3.6
                                  seq LAVLLVLFTLNIL/KS

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:


Met Trp Tyr Leu Ala Val Leu Leu Val Leu Phe Thr Leu Asn Ile Leu
    -15                 -10                 -5

Lys Ser Leu Tyr Trp Gln Pro Gly
 1               5



 (2) INFORMATION FOR SEQ ID NO: 499:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 58 amino acids
          (B) TYPE: AMINO ACID
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Brain

    (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: -42..-1
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 3.5
                                  seq INSLLEXSSLSRC/LE

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:


Met Phe Thr Phe Gly Arg Leu Phe Gln Ile Ile Thr Val Val Thr Cys
      -40                 -35                 -30

Leu Gln Phe Ile Gln Asp Cys Cys Ile His Ser Arg Gln Ile Asn Ser
    -25                 -20                 -15

Leu Leu Glu Xaa Ser Ser Leu Ser Arg Cys Leu Glu Val Pro Met Tyr
-10                 -5                  1               5
```

```
Val Lys Cys Ile Gly Ser Lys Ile Pro Leu
            10                    15
```

(2) INFORMATION FOR SEQ ID NO: 500:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -51..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 3.5
                            seq VGTLCQLDWWIWG/GI

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```
Met Ile Gln Asp Arg Asp Arg Cys Ala Gln Ala Ala Ala Val Ala Ala
    -50               -45                   -40

Val Gly Asn Leu Glu Pro Arg Gly Thr Pro Gly Pro Glu Asp Glu Ala
-35               -30                   -25                   -20

Phe Cys Leu Pro Gly Cys Val Gly Thr Leu Cys Gln Leu Asp Trp Trp
              -15                   -10                   -5

Ile Trp Gly Gly Ile His Pro His Pro Thr Arg Lys Ala Trp
          1           5                   10
```

(2) INFORMATION FOR SEQ ID NO: 501:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 amino acids
        (B) TYPE: AMINO ACID
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: PROTEIN

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Brain

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: -31..-1
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION: score 11.3

seq LLLCLLWIGYSQG/TT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Lys Ile Ile Phe Pro Ile Leu Ser Asn Pro Val Phe Arg Arg Thr
    -30   -25   -20
Val Lys Leu Leu Leu Cys Leu Leu Trp Ile Gly Tyr Ser Gln Gly Thr
    -15   -10   -5   1
Thr His Val Leu Arg Phe Gly Gly Ile Phe Glu Tyr Val Glu Ser Gly
              5   10   15

(2) INFORMATION FOR SEQ ID NO: 502:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 57 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Brain

        (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: -26..-1
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION: score 6.6
                                    seq LFWLASGWTPAFA/YS

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Val Ser Arg Met Val Ser Thr Met Leu Ser Gly Leu Leu Phe Trp
    -25   -20   -15
Leu Ala Ser Gly Trp Thr Pro Ala Phe Ala Tyr Ser Pro Arg Thr Pro
    -10   -5   1   5
Asp Arg Val Ser Glu Ala Asp Ile Gln Arg Leu Leu His Gly Val Met
              10   15   20
Glu Gln Leu Gly Ile Ala Arg Pro Arg
          25   30

(2) INFORMATION FOR SEQ ID NO: 503:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 46 amino acids
            (B) TYPE: AMINO ACID
            (D) TOPOLOGY: LINEAR

        (ii) MOLECULE TYPE: PROTEIN

```
(vi) ORIGINAL SOURCE:
     (A) ORGANISM: Homo Sapiens
     (F) TISSUE TYPE: Brain

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: -24..-1
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION: score 4.8
                            seq ATMVSGSSGLAXA/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:


Met Thr Ala Thr Leu Ala Ala Ala Ala Asp Ile Ala Thr Met Val Ser
              -20             -15                  -10

Gly Ser Ser Gly Leu Ala Xaa Ala Arg Leu Leu Ser Arg Xaa Ser Ser
              -5                  1                  5

Cys Arg Arg Met Glu Phe Gly Ile Val Pro Thr Gln Pro Arg
     10              15                  20
```